

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:07:22 ; Search time 95 Seconds

(without alignments)
43.461 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 ELKCYCKEPMISAAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_invertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	63.0	790	4 Q96MR9	Q96mr9 homo sapien
2	52	56.5	127	11 Q9DD23	Q9dd23 mus musculus
3	52	56.5	2841	5 Q8MLU9	Q8mlu9 drosophila
4	52	56.5	2931	5 Q9W2C6	Q9w2c6 drosophila
5	50	54.3	955	4 Q96DN2	Q96dn2 homo sapien
6	48.5	52.7	268	5 Q8MQH9	Q8mqh9 paracentrot
7	48	52.2	191	11 Q8BLC7	Q8blc7 mus musculus
8	48	52.2	240	11 Q9JLK8	Q9jlk8 mus musculus
9	48	52.2	243	4 Q9H163	Q9h163 homo sapien
10	48	52.2	243	11 Q9D0V2	Q9d0v2 mus musculus
11	48	52.2	243	11 Q8BLR4	Q8blr4 mus musculus
12	48	52.2	462	10 Q8L7I2	Q8l7i2 arabidopsis
13	48	52.2	773	4 Q9H164	Q9h164 homo sapien
14	48	52.2	773	11 Q9QYF3	Q9qyf3 mus musculus
15	48	52.2	776	11 Q9JIT4	Q9jit4 mus musculus
16	48	52.2	797	4 Q9H3G9	Q9h3g9 homo sapien

17 48 52.2 800 4 Q96JL6
18 48 52.2 835 4 Q9H165
19 48 52.2 889 10 Q9FHH9
20 47 51.1 129 11 Q920G7
21 47 51.1 367 2 Q9AJ67
22 47 51.1 472 16 Q9KFS9
23 46 50.0 225 17 Q29808
24 45 48.9 157 17 Q29312
25 45 48.9 443 11 Q8BLX6
26 45 48.9 484 10 Q9FEL7
27 45 48.9 1209 12 Q8JME0
28 44 47.8 100 17 Q97BHS
29 44 47.8 134 11 Q83318
30 44 47.8 148 12 Q56946
31 44 47.8 366 10 Q8S6L7
32 44 47.8 388 5 Q17002
33 44 47.8 391 16 Q9KCP4
34 44 47.8 565 5 Q04134
35 43 46.7 61 4 Q8TE66
36 43 46.7 70 11 Q54837
37 43 46.7 114 16 Q8YPM3
38 43 46.7 148 5 Q9VLF3
39 43 46.7 150 5 Q8MT42
40 43 46.7 204 5 Q811A3
41 43 46.7 267 16 Q8RFU1
42 43 46.7 295 5 Q8MQB4
43 43 46.7 295 16 Q8FFA1
44 43 46.7 413 16 Q8XHM2
45 43 46.7 449 10 Q8W047

ALIGNMENTS

RESULT 1

Q96MR9 ID Q96MR9 PRELIMINARY; PRT; 790 AA.
AC Q96MR9
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein FLJ31986.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AK056548; BAB71213.1; --
DR InterPro: IPR001509; KRAB.
DR InterPro: IPR006895; zf-Sec23_Sec34.
DR InterPro: IPR007087; Znf C2H2.
DR Pfam: PF01352; KRAB; 2.
DR Pfam: PF00096; zf-C2H2; 14.
DR Pfam: PF04810; zf-Sec23_Sec24; 1.
DR SMART: SM00349; KRAB; 2.
DR SMART: SM00355; Znf C2H2; 14.
DR PROSITE: PS00805; KRAB; 2.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 13.
DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 14.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 790 AA; 91134 MW; BID7B3CC07C1179F CRC64;

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Query Match      63.0%; Score 58; DB 4; Length 790;
Best Local Similarity 64.3%; Pred. No. 0.14;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KCVYCKEPTWTSAC 16
DB 517 KCVYCKGKPTFTSSAC 530

RESULT 2
Q9DD23 PRELIMINARY; PRT; 127 AA.
AC Q9DD23
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE 0610005K03Rik protein.
GN 0610005K03Rik
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawaji Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK002226; BAB21948.1; --
DR HSSP; P13987; 1ERG.
DR MGD; MGI:1915561; 0610005K03Rik.
DR InterPro; IPR003632; LY-6_CD59.
DR InterPro; IPR001526; LY6_UPAR.
DR Jfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; LY-6_CD59; 1.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 127 AA; 13279 MW; 9CCE20688671982C CRC64;

Query Match      56.5%; Score 52; DB 11; Length 127;
Best Local Similarity 46.7%; Pred. No. 0.31;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LKCVYCKEPTWTSAC 16
DB 23 LQCVTCANPVSASNC 37

RESULT 3
Q8MLU9 PRELIMINARY; PRT; 2841 AA.
AC Q8MLU9
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE CG13492-PB.

```

GN Drosophila melanogaster (Fruit fly).

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hoskin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasio P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195 (2000).

[2]

RP SEQUENCE FROM N.A.

RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

RA Banron J., An H., Baldwin D., Banzone J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]

RP SEQUENCE FROM N.A.

RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,

RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,

RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,

```

RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003455; AAM71018.1; -.
DR FlyBase; FBgn0034662; CG13492.
DR InterPro; IPR000173; CAP_dhdrogenase.
DR PROSITE; PS00071; GAPD; 1.
SQ SEQUENCE 2841 AA; 306647 MW; 21E2A1B14455D494 CRC64;

Query Match 56.5%; Score 52; DB 5; Length 2841;
Best Local Similarity 47.4%; Pred. No. 4;
Matches 9; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 2 LKCYTCKEPM-----TSAAC 16
|:|||||:|:|
Db 1321 LECYTKDPFCEDPTTSC 1339

RESULT 4
Q9W2C6 PRELIMINARY; PRT; 2931 AA.
ID Q9W2C6
AC Q9W2C6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG13492 protein.
GN CG13492.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003455; AAF46766.2; -.
DR FlyBase; FBgn0034662; CG13492.
DR InterPro; IPR000173; CAP_dhdrogenase.
DR PROSITE; PS00071; GAPD; 1.
SQ SEQUENCE 2931 AA; 316518 MW; B06C15D9DF257EF6 CRC64;

Query Match 56.5%; Score 52; DB 5; Length 2931;
Best Local Similarity 47.4%; Pred. No. 4;
Matches 9; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 2 LKCYTCKEPM-----TSAAC 16
|:|||||:|:|
Db 1411 LECYTKDPFCEDPTTSC 1429

RESULT 5
Q96DN2 PRELIMINARY; PRT; 955 AA.
ID Q96DN2
AC Q96DN2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ32009.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Makamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuho K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056571; BAB71219.1; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001007; WVF_C.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00093; vwc; 5.
DR SMART; SM00179; EGF_Ca; 3.
DR SMART; SM00214; VMC; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 3.
DR PROSITE; PS01208; WVF_C; 5.
KW Hypothetical protein; EGF-like domain.
SQ SEQUENCE 955 AA; 99884 MW; 88B0DCA8AABA9188 CRC64;

Query Match 54.3%; Score 50; DB 4; Length 955;
Best Local Similarity 53.8%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPM-----TSAAC 16
|:|||||:|:|

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Db 556 CFTCQPTPTGTC 568

RESULT 6

Q8MOH9 PRELIMINARY; PRT; 268 AA.
 AC Q8MOH9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE An1 protein (Fragment).
 OS Paracentrotus lividus (Common sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
 OC Paracentrotus.
 OK NCBI_TaxID=7656;
 [1]
 RP SEQUENCE FROM N.A.
 RA Di Carlo M., Dalmazio S., Montana G., Romancino D.P.;
 RT "Animal-vegetal mRNA localization.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY130251; AAM78147.1; -.
 FT NON TR 1
 SQ SEQUENCE 268 AA; 31151 MW; 3D861B07112AFFFS CRC64;

Query Match 52.7%; Score 48.5; DB 5; Length 268;
 Best Local Similarity 47.4%; Pred. No. 2.2;
 Matches 9; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

Qy 3 KCYTCK-----EPMTSAAC 16
 |||||:|||||
 Db 199 KCFTCRNNKHSEPTSPNC 217

RESULT 7

Q8BLC7 PRELIMINARY; PRT; 191 AA.
 AC Q8BLC7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE B-cell CLL/lymphoma 11A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK045556; BAC32416.1; -.
 SQ SEQUENCE 191 AA; 21075 MW; 23B17797A92CF20B CRC64;

Query Match 52.2%; Score 48; DB 11; Length 191;
 Best Local Similarity 72.7%; Pred. No. 2.1;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CYTCKEPTMTSA 14
 |||||:|||||
 Db 120 CTTCKQPFTSA 130

RESULT 8

Q9JLK8 PRELIMINARY; PRT; 240 AA.
 AC Q9JLK8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ecotropic viral integration site 9 isoform C.
 GN BCL11A OR EVI9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20221564; PubMed=10757802;
 RA Nakamura T., Yamazaki Y., Saiki Y., Moriyama M., Largaespada D.A.,
 RA Jenkins N.A., Copeland N.G.;
 RT "Evi9 encodes a novel zinc finger protein that physically interacts
 RT with BCL6, a known human B-cell proto-oncogene product.";
 RL Mol. Cell. Biol. 20:3178-3186 (2000).
 DR EMBL; AF169037; AA565929.1; -.
 DR MGD; MGI:106190; Bcl11a.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 240 AA; 26511 MW; 569B5B4CC3D21F2F CRC64;

Query Match 52.2%; Score 48; DB 11; Length 240;
 Best Local Similarity 72.7%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CYTCKEPTMTSA 14
 |||||:|||||
 Db 172 CTTCKQPFTSA 182

RESULT 9

Q9HI63 PRELIMINARY; PRT; 243 AA.
 AC Q9HI63;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE B-cell lymphoma/leukaemia 11A short form.
 GN BCL11A-S.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Satterwhite E., Sonoki T., Willis T.G., Siebert R.;
 RT "The BCL11 gene family: involvement of BCL11A in Hodgkin's and non-
 RT Hodgkin's lymphomas.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ404613; CAC17725.1; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.
 KW B-cell; Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 243 AA; 26965 MW; 5B24E211FAP30726 CRC64;

Query Match 52.2%; Score 48; DB 4; Length 243;
 Best Local Similarity 72.7%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CYTCKEPTMTSA 14
 |||||:|||||
 Db 172 CTTCKQPFTSA 182

RESULT 10
 Q9D0V2

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ID Q9D0V2 PRELIMINARY; PRT; 243 AA.
AC Q9D0V2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 18 days embryo cDNA, RIKEN full-length enriched library,
DE clone.1110067K14, full insert sequence.
DE BCL11A OR EV19.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RL ENBL: AK004395; BAB23285.1;
DR MGD; MGI:106190; Bcl11a.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF00096; zf-C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 243 AA; 26823 MW; B18CC391B83BC479 CRC64;

Query Match 52.2%; Score 48; DB 11; Length 243;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CYTCKEPTSA 14
Db 172 CTTCKQPTSA 182

RESULT 11
Q9BLR4 PRELIMINARY; PRT; 243 AA.
ID Q9BLR4;
AC Q9BLR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-cell CLL/lymphoma 11A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;

QY 1 ELKCYTCKEPTSA 15
Db 292 ELKCPCKEVMKDA 306

RESULT 13
Q9H164 PRELIMINARY; PRT; 773 AA.
ID Q9H164;
AC Q9H164;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-cell lymphoma/leukaemia 11A long form.
GN BCL11A-L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Satterwhite E., Sonoki T., Willis T.G., Siebert R.;
RX "The BCL11 gene family: involvement of BCL11A in Hodgkin's and non-
RT Hodgkin's lymphomas.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

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RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL: AK043677; BAC31616.1;
SQ SEQUENCE 243 AA; 26823 MW; B19C19FD90473679 CRC64;

Query Match 52.2%; Score 48; DB 11; Length 243;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CYTCKEPTSA 14
Db 172 CTTCKQPTSA 182

RESULT 12
Q8L7L2 PRELIMINARY; PRT; 462 AA.
ID Q8L7L2;
AC Q8L7L2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE DNA-binding protein-like (Fragment).
GN AT5G47430.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL: AV128390; AAM91593.1;
DR InterPro: IPR001878; Znf_CCHC.
DR PRINTS; PR00939; C2HCZNFINGER.
KW DNA-binding.
FT NON TER 462
SQ SEQUENCE 462 AA; 50377 MW; 84EA259DFB3D564C CRC64;

Query Match 52.2%; Score 48; DB 10; Length 462;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELKCYTCKEPTSA 15
Db 292 ELKCPCKEVMKDA 306

RESULT 13
Q9H164 PRELIMINARY; PRT; 773 AA.
ID Q9H164;
AC Q9H164;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-cell lymphoma/leukaemia 11A long form.
GN BCL11A-L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Satterwhite E., Sonoki T., Willis T.G., Siebert R.;
RX "The BCL11 gene family: involvement of BCL11A in Hodgkin's and non-
RT Hodgkin's lymphomas.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AJ404612; CAC17724.1; -.
DR InterPro; IPR007087; Znf C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR SMART; SM00355; Znf C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
DR B-cell; Metal-binding; Zinc; Zinc-finger.
KW SEQUENCE 773 AA; 83993 MW; 1F8A6A0DBF45AB1E CRC64;

Query Match          52.2%; Score 48; DB 4; Length 773;
Best Local Similarity 72.7%; Pred. No. 6.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CYTCKEPM TSA 14
Db 172 CTCKQP TSA 182

RESULT 14
Q9QYE3 PRELIMINARY; PRT; 773 AA.
AC Q9QYE3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE C2H2-type zinc finger protein.
GN BCL11A OR EVI9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BXH/2;
RX MEDLINE=20221564; PubMed=10757802;
RA Nakamura T., Yamazaki Y., Saiki Y., Moriyama M., Largaespada D.A.,
RA Jenkins N.A., Copeland N.G.;
RT "Evi9 encodes a novel zinc finger protein that physically interacts
RT with BCL6, a known human B-cell proto-oncogene product.";
RL Mol. Cell. Biol. 20:3178-3186(2000).
DR EMBL; AF051525; AAF22430.1; -.
DR MGD; MGI:106190; Bcl11a.
DR InterPro; IPR007087; Znf C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR SMART; SM00355; Znf C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 773 AA; 83855 MW; 3BD10B7F14AA9EC4 CRC64;

Query Match          52.2%; Score 48; DB 11; Length 773;
Best Local Similarity 72.7%; Pred. No. 6.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CYTCKEPM TSA 14
Db 172 CTCKQP TSA 182

RESULT 15
Q9JIT4 PRELIMINARY; PRT; 776 AA.
AC Q9JIT4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CTIP1 protein.
GN BCL11A OR CTIP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=20209406; PubMed=10744719;
RA Avram D., Fields A., Pretty On Top K., Nevriy D.J., Ishmael J.E.,
RA Leid M.;
RT "Isolation of a novel family of C(2)H(2) zinc finger proteins
RT implicated in transcriptional repression mediated by chicken ovalbumin
RT upstream promoter transcription factor (COUP-Tf) orphan nuclear
RT receptors.";
RL J. Biol. Chem. 275:10315-10322(2000).
DR EMBL; AF186018; AAF63682.1; -.
DR MGD; MGI:106190; Bcl11a.
DR InterPro; IPR007087; Znf C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR SMART; SM00355; Znf C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 776 AA; 84116 MW; FBF388B7A03787A0 CRC64;

Query Match          52.2%; Score 48; DB 11; Length 776;
Best Local Similarity 72.7%; Pred. No. 6.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CYTCKEPM TSA 14
Db 172 CTCKQP TSA 182

Search completed: October 9, 2003, 14:11:55
Job time : 99 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:04:11 ; Search time 23 Seconds
(without alignments)
32.714 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 ELKCYCKEPTMTSAAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	91.3	103	1 SLUR_HUMAN	P50000 homo sapien
2	47	51.1	110	1 SLUR_MOUSE	Q320K7 mus musculu
3	45	48.9	153	1 VE6_HPV10	P36809 human papil
4	44	47.8	126	1 CD59_RAT	P27274 rattus norv
5	44	47.8	224	1 MAUM_PARDE	Q51659 paracoccus
6	43	46.7	61	1 MT1A_HUMAN	P04731 homo sapien
7	43	46.7	154	1 VE6_HPV53	P36815 human papil
8	43	46.7	155	1 VE6_HPV56	P24836 human papil
9	43	46.7	295	1 EUTC_ECO57	Q8XEH3 escherichia
10	43	46.7	295	1 EUTC_ECOL6	Q8F1A1 escherichia
11	43	46.7	295	1 EUTC_ECOL1	P19636 escherichia
12	43	46.7	365	1 P43_XENBO	P25066 xenopus bor
13	43	46.7	365	1 P43_XENLA	P25456 xenopus lae
14	43	46.7	469	1 APTD_DROME	P29673 drosophila
15	42	45.7	394	1 FDHB_MENTF	Q50570 methanobact
16	42	45.7	572	1 ZYX_HUMAN	Q15942 homo sapien
17	42	45.7	803	1 UBPE_YEAST	P38237 saccharomyc
18	41	44.6	126	1 CD59_PAPSP	Q28785 papio sp. (
19	41	44.6	149	1 VE6_HPV33	P06427 human papil
20	41	44.6	279	1 SLI3_MOUSE	Q70433 mus musculu
21	41	44.6	279	1 SLI3_RAT	C35115 rattus norv
22	41	44.6	399	1 FDHB_METFO	P06130 methanobact
23	41	44.6	495	1 MLPT_DROME	Q24400 drosophila
24	41	44.6	3133	1 HMC7_BOMMO	P98092 bombyx mori
25	40	43.5	58	1 CTC7_HUMAN	Q93082 homo sapien
26	40	43.5	61	1 MT1R_HUMAN	Q93083 homo sapien
27	40	43.5	61	1 MT2_CRIGR	P02799 cricetus
28	40	43.5	61	1 MT2_MESRU	P17808 mesocricetu
29	40	43.5	123	1 PSCA_HUMAN	Q43653 homo sapien
30	40	43.5	123	1 PSCA_MOUSE	P57096 mus musculu
31	40	43.5	128	1 CD59_CALSQ	P46657 callithrix
32	40	43.5	128	1 CD59_CERAE	Q28216 cercopithec
33	40	43.5	249	1 MOEB_SALTY	Q56067 salmonella

RESULT 1

SLURP_HUMAN	STANDARD;	PRT;	103 AA.
ID	SLURP_HUMAN		
AC	P50000; Q92483;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Secreted Ly-6/uPAR related protein 1 precursor (SLURP-1) (ARS component B) (ARS(component B)-81/S) (Anti-neoplastic urinary protein) (ANUP).		
DE	SLURP1 OR ARS.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Placenta;		
RA	Mastrangeli R.;		
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE OF 22-36.		
RC	TISSUE=Granulocyte;		
RX	MEDLINE=96351837; PubMed=8742060;		
RA	Ridge R.J., Sloane N.H.;		
RT	"Partial N-terminal amino acid sequence of the anti-neoplastic urinary protein (ANUP) and the anti-tumour effect of the N-terminal nonapeptide of the unique cytokine present in human granulocytes.";		
RT	Cytokine 8:1-5(1996).		
RN	[3]		
RP	PARTIAL SEQUENCE.		
RA	MEDLINE=99226809; PubMed=10211827;		
RA	Andermann K., Wattler F., Wattler S., Heine G., Meyer M., Forsgmann W.-G., Nehls M.;		
RT	"Structural and phylogenetic characterization of human SLURP-1, the first secreted mammalian member of the Ly-6/uPAR protein superfamily.";		
RT	Protein Sci. 8:810-819(1999).		
RN	[4]		
RP	DISEASE.		
RX	MEDLINE=21181711; PubMed=11285253;		
RA	Fischer J., Bouadjir B., Heilig R., Huber M., Lefevre C., Jobard F., Macari F., Bakija-Konsuo A., Ait-Belkacem F., Weissenbach J., Lathrop M., Hohl D., Prud'homme J.-F.;		
RT	"Mutations in the gene encoding SLURP-1 in Mal de Meleda.";		
RL	Hum. Mol. Genet. 10:875-880(2001).		
CC	-1- FUNCTION: Has an antitumor activity.		
CC	-1- SUBUNIT: Homodimer.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- TISSUE SPECIFICITY: GRANULOCYTES. EXPRESSED IN SKIN.		
CC	-1- DISEASE: Defects in SLURP1 are a cause of Mal de Meleda (MDM), a rare autosomal recessive skin disorder, characterized by transgressive palmo-plantar keratoderma (PPK), keratotic skin lesions, perioral erythema, brachydactyly and nail abnormalities.		
CC	-1- SIMILARITY: Contains 1 UPAR/Ly6 domain.		
CC	-1- CAUTION: IT IS NOT CERTAIN THAT ARS AND ANUP ARE IDENTICAL.		

Q21230 caenorhabdi
P44539 haemophilus
Q9va72 aeropyrum p
P06757 rattus norv
Q856m9 thermoanaer
P53708 homo sapien
P04050 saccharomyc
O56075 p genome po
P01306 gallus gall
P35461 mus musculu
P51447 actus trivi
P06931 bovine papi

ALIGNMENTS

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalta D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE TRANSCRIPTICALLY REGULATED BY BOTH HEAVY METALS AND GLUCOCORTICOIDS.
-!- SUBUNIT: Monomer.
-!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS: FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11 CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.

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Query Match	47.8%;	Score 44;	DB 1;	Length 224;
Best Local Similarity	43.8%;	Pred. NO. 4.6;		
Matches	7;	Conservative	3;	Mismatches 6; Indels 0; Gaps 0;
OY	1	ELKCYCKEPMPTSAAC 16		
DB	99	EVPCYNCKDVPACARAC 114		
RESULT 6				
MTIA_HUMAN				
ID	MTIA_HUMAN	STANDARD;	PRT;	61 AA.
AC	P04731;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DE	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Metallothionein-IA (MT-IA).			
GN	MTIA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84205649; PubMed=6327055;			
RA	Richards R.I., Heguy A., Karin M.;			
RT	"Structural and functional analysis of the human metallothionein-IA			
RT	gene: differential induction by metal ions and glucocorticoids."			
RL	Cell 37:263-272(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Liver;			
RA	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			

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FT METAL 60 60 CLUSTER A.
SQ SEQUENCE 61 AA; 6133 MW; 8FBA68BEA56B6A13 CRC64;

Query Match 46.7%; Score 43; DB 1; Length 61;
Best Local Similarity 40.9%; Pred. No. 1.8;
Matches 9; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

QY 1 ELKCYTCKE-----PMTSAAC 16
Db 23 ECKNSCKKSCCCCPMSCAKC 44

RESULT 7
VE6_HPV53
ID -V56_HPV53 STANDARD; PRT; 154 AA.
AC P36815;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 53.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X74483; CAAS2591.1; --
CC FIR; S36527; S36527.
CC InterPro; IPR001334; E6.
CC Pfam; PF00518; E6; 1.
CC DR Early protein; DNA-binding; Nuclear protein; Zinc-finger;
CC KW Oncogene.
CC FT ZN_FING 34 70
CC ZN_FING 107 143 POTENTIAL.
CC SQ SEQUENCE 154 AA; 18168 MW; 68A426704546010C CRC64;

Query Match 46.7%; Score 43; DB 1; Length 154;
Best Local Similarity 45.5%; Pred. No. 4.5;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMT 12
Db 105 IRCYRCQSPMT 115

RESULT 8
ID -V56_HPV56 STANDARD; PRT; 155 AA.
AC P24836;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 56.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.

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OX NCBI_TaxID=10596;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90063558; PubMed=2555440;
RA Loerincz A.T., Quinn A.P., Goldeborough M.D., McAllister P.,
RA Temple G.P.;
RT "Human papillomavirus type 56: a new virus detected in cervical
RT cancers.";
RL J. Gen. Virol. 70:3099-3104(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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CC
CC EMBL; X74483; CAAS2596.1; --
CC FIR; A33377; W6WL56.
CC InterPro; IPR001334; E6.
CC Pfam; PF00518; E6; 1.
CC DR Early protein; DNA-binding; Nuclear protein; Zinc-finger;
CC KW Oncogene.
CC FT ZN_FING 33 69
CC ZN_FING 106 142 POTENTIAL.
CC SQ SEQUENCE 155 AA; 18524 MW; E8732949398B4C4B CRC64;

Query Match 46.7%; Score 43; DB 1; Length 155;
Best Local Similarity 45.5%; Pred. No. 4.6;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMT 12
Db 104 IRCYRCQSPMT 114

RESULT 9
ID -EUTC_ECO57 STANDARD; PRT; 295 AA.
AC Q8XEH3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ethanalamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanalamine
DE ammonia-lyase small subunit).
GN EUTC OR Z3705 OR ECS3311.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Ferra N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).

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RN RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasekawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- CATALYTIC ACTIVITY: Ethanolamine = acetaldehyde + NH(3).
CC -!- COFACTOR: Adenosylcobalamin (By similarity).
CC -!- PATHWAY: Ethanolamine utilization.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -!- SIMILARITY: Belongs to the eutC family.
CC
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CC
DR EMBL; AE005474; AAG57558.1; -.
DR EMBL; AP002561; BAB36734.1; -.
DR PIR; B85887; B85887.
DR PIR; G91042; G91042.
DR HANAP; MF 00601; -.
DR Lyase; Cofact; Complete proteome.
KW CONFLICT 82 82 R -> H (IN REF. 2).
FT
SQ SEQUENCE 295 AA; 31812 MW; 3D55EAD80374A1D CRC64;

Query Match 46.7%; Score 43; DB 1; Length 295;
Best Local Similarity 50.0%; Pred. No. 8.6;
Matches 9; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Oy 1 ELKC--YTCKEPMTSAAC 16
Db 26 EAKCATTTCAAPVTISEC 43

RESULT 10
EUTC_ECOL6
ID EUTC_ECOL6 STANDARD; PRT; 295 AA.
AC Q8PFA1;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ethanolamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanolamine
DE ammonia-lyase small subunit).
GN EUTC OR C2974.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22389234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- CATALYTIC ACTIVITY: Ethanolamine = acetaldehyde + NH(3).
CC -!- COFACTOR: Adenosylcobalamin (By similarity).
CC -!- PATHWAY: Ethanolamine utilization.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By

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CC similarity).
CC -!- SIMILARITY: Belongs to the eutC family.
CC
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CC
DR EMBL; AE016764; AAN81424.1; -.
DR HANAP; MF 00601; -.
DR Lyase; Cofact; Complete proteome.
SQ SEQUENCE 295 AA; 31811 MW; B07601450F8B20EA CRC64;

Query Match 46.7%; Score 43; DB 1; Length 295;
Best Local Similarity 50.0%; Pred. No. 8.6;
Matches 9; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Oy 1 ELKCVT--CKEPMPTSAAC 16
Db 26 EAKCATTTCAAPVTISEC 43

RESULT 11
EUTC_ECOL1
ID EUTC_ECOL1 STANDARD; PRT; 295 AA.
AC P19636; P78273;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ethanolamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanolamine
DE ammonia-lyase small subunit).
GN EUTC OR B2440.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satchi Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yanagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN
RP SEQUENCE OF 1-15.
RX MEDLINE=90324235; PubMed=2197274;
RA Faust L.R.P., Connor J.A., Roof D.M., Hoch J.A., Babior B.M.;
RT "Cloning, sequencing, and expression of the genes encoding the
RT adenosylcobalamin-dependent ethanolamine ammonia-lyase of Salmonella
RT typhimurium";
RL J. Biol. Chem. 265:12462-12466(1990).
CC -!- CATALYTIC ACTIVITY: Ethanolamine = acetaldehyde + NH(3).
CC -!- COFACTOR: Adenosylcobalamin.

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CC -|- PATHWAY: Ethanolamine utilization.
CC -|- SUBUNIT: Heterodimer of a small and a large subunit.
CC -|- SIMILARITY: Belongs to the eutC family.
CC
CC -----
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CC -----
CC EMBL; AE000331; AAC75493.1; -.
CC DR EMBL; D90873; BAA16322.1; -.
CC DR EMBL; D90874; BAA16328.1; -.
CC DR PIR; G65018; G65018.
CC DR ECGene; EG50007; eutC.
CC DR HAMAP; MF 00601; -. 1.
CC KW Lyase; Cobalt; Complete proteome.
CC SQ SEQUENCE 295 AA; 31781 MW; C7E87143B8E050E5 CRC64;
CC
CC Query Match 46.7%; Score 43; DB 1; Length 295;
CC Best Local Similarity 50.0%; Pred. No. 8.6;
CC Matches 9; Conservative 2; Mismatches 5; Indels 2; Gaps 1;
CC
CC QY 1 ELKCYT--CKEPTMSAAC 16
CC DB 26 EAKCATTNCAAPVTSSC 43
CC
CC RESULT 12
CC P43_XENBO
CC ID P43_XENBO STANDARD; PRT; 365 AA.
CC AC P25066;
CC DT 01-MAY-1992 (Rel. 22, Created)
CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE P43 5S RNA binding protein (42S P43) (Theaurin B).
CC OS Xenopus borealis (kenyan clawed frog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
CC OC Xenopodinae; Xenopus.
CC OX NCBI_TaxID=8354;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=90235278; PubMed=2331751;
CC RA Joho K.E., Darby M.K., Crawford E.T., Brown D.D.;
CC RT "A finger protein structurally similar to TFIIA that binds
CC RT exclusively to 5S RNA in Xenopus.";
CC RL Cell 61:293-300(1990).
CC CC -|- FUNCTION: P43 IS A 5S RNA BINDING PROTEIN WHICH IS A MAJOR
CC CC CONSTITUENT OF OOCYTES AND COMPRISES PART OF A 42S
CC CC RIBONUCLEOPROTEIN STORAGE PARTICLE.
CC CC -|- SUBUNIT: THE 42S RNP PARTICLE COMPRISES FOUR SUBUNITS EACH OF
CC CC TWO MOLECULES OF P50 (E1-ALPHA) AND ONE MOLECULE OF THE 5S RNA
CC CC BINDING PROTEIN 43.
CC CC -|- SIMILARITY: Contains 9 C2H2-type zinc fingers.
CC -----
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CC -----
CC EMBL; M32471; AAA49712.1; -.
CC DR PIR; A34895; A34895.
CC DR InterPro; IPR007087; Znf_C2H2.
CC DR Pfam; PF00096; zf-C2H2; 9.
CC DR SMART; SM00355; Znf_C2H2; 9.
CC DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
CC DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
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DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
KW Zinc-finger; Metal-binding; RNA-binding; Repeat.
FT ZN_FING 15 39 C2H2-TYPE 1.
FT ZN_FING 45 69 C2H2-TYPE 2.
FT ZN_FING 75 100 C2H2-TYPE 3.
FT ZN_FING 106 130 C2H2-TYPE 4.
FT ZN_FING 136 160 C2H2-TYPE 5.
FT ZN_FING 163 187 C2H2-TYPE 6.
FT ZN_FING 191 213 C2H2-TYPE 7.
FT ZN_FING 220 245 C2H2-TYPE 8.
FT ZN_FING 251 275 C2H2-TYPE 9.
SQ SEQUENCE 365 AA; 41726 MW; D7E8C76B80E42BF2 CRC64;
CC
CC Query Match 46.7%; Score 43; DB 1; Length 365;
CC Best Local Similarity 46.7%; Pred. No. 11;
CC Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 1 ELKCYTCKEPTMSAA 15
CC DB 190 ELQCAACKRPFKAS 204
CC
CC RESULT 13
CC P43_XENLA
CC ID P43_XENLA STANDARD; PRT; 365 AA.
CC AC P25456;
CC DT 01-MAY-1992 (Rel. 22, Created)
CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE P43 5S RNA binding protein (42S P43) (Theaurin B).
CC OS Xenopus laevis (African clawed frog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
CC OC Xenopodinae; Xenopus.
CC OX NCBI_TaxID=8355;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=90235278; PubMed=2331751;
CC RA Joho K.E., Darby M.K., Crawford E.T., Brown D.D.;
CC RT "A finger protein structurally similar to TFIIA that binds
CC RT exclusively to 5S RNA in Xenopus.";
CC RL Cell 61:293-300(1990).
CC CC -|- FUNCTION: P43 IS A 5S RNA BINDING PROTEIN WHICH IS A MAJOR
CC CC CONSTITUENT OF OOCYTES AND COMPRISES PART OF A 42S
CC CC RIBONUCLEOPROTEIN STORAGE PARTICLE.
CC CC -|- SUBUNIT: THE 42S RNP PARTICLE COMPRISES FOUR SUBUNITS EACH OF
CC CC TWO MOLECULES OF P50 (E1-ALPHA) AND ONE MOLECULE OF THE 5S RNA
CC CC BINDING PROTEIN 43.
CC -----
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CC -----
CC EMBL; M32473; AAA49714.1; -.
CC DR HSP; P03001; ITF3.
CC DR InterPro; IPR007087; Znf_C2H2.
CC DR Pfam; PF00096; zf-C2H2; 9.
CC DR SMART; SM00355; Znf_C2H2; 9.
CC DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
CC DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 7.
CC KW Zinc-finger; Metal-binding; RNA-binding; Repeat.
CC FT ZN_FING 15 39 C2H2-TYPE.
CC FT ZN_FING 45 69 C2H2-TYPE.
CC FT ZN_FING 75 100 C2H2-TYPE.
CC FT ZN_FING 106 130 C2H2-TYPE.
CC FT ZN_FING 136 160 C2H2-TYPE.
CC FT ZN_FING 163 187 C2H2-TYPE.
CC FT ZN_FING 191 213 C2H2-TYPE.
```

FT ZN FING 220 245 C2H2-TYPE.
 FT ZN FING 251 275 C2H2-TYPE.
 SQ SEQUENCE 365 AA; 41694 MW; 2B5B6607192995 CRC64;

Query Match 46.7%; Score 43; DB 1; Length 365;
 Best Local Similarity 46.7%; Pred. No. 11;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELKCYTCCKEPTMSAA 15
 ||| ||| ||| :
 Db 190 ELQCAACKPKKAS 204

RESULT 14
 ID APTE DROME STANDARD; PRT; 469 AA.
 AC P29673; Q9V9H5;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apterous protein.
 GN AP OR CG8376.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RX MEDLINE=9249766; PubMed=1349545;
 RA Cohen B., McGuffin M.E., Pfeifle C., Segal D., Cohen S.M.;
 "Apterous, a gene required for imaginal disc development in
 RT Drosophila encodes a member of the LIM family of developmental
 RT regulatory proteins.";
 RL Genes Dev. 6:715-729(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92398973; PubMed=1524829;
 RA Bourguin C., Lundgren S.E., Thomas J.B.;
 RT "Apterous is a Drosophila LIM domain gene required for the
 RT development of a subset of embryonic muscles.";
 RN Neuron 9:549-561(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burtis K., Busan D.A., Butler H., Cackley E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei E., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RL -1- FUNCTION: REQUIRED FOR THE NORMAL DEVELOPMENT OF THE WING AND
 CC HALTER IMAGINAL DISKS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PNS AND CNS.
 CC -1- SIMILARITY: Contains 1 homeobox domain.
 CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
 CC -----
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 CC -----
 DR EMBL; X65158; CAA46276.1; -;
 DR EMBL; M82841; AAA28673.1; -;
 DR EMBL; AS003785; AAM68357.1; -;
 DR PIR; JH0718; JH0718.
 DR HSP; P32965; ICTL.
 DR TRANSFAC; T01074; -;
 DR FlyBase; FBgn0000099; ap.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0007411; P:axon guidance; IMP.
 DR GO; GO:0007559; P:histolysis; IMP.
 DR GO; GO:0007479; P:leg disc proximal/distal pattern formation; IMP.
 DR GO; GO:0007517; P:leg disc development; IMP.
 DR GO; GO:0007399; P:neurogenesis; IMP.
 DR GO; GO:0006350; P:transcription; IMP.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR001781; LIM.
 DR InterPro; IPR007107; LIM homeo.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00412; LIM; 2.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000094; LIM; 2.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00132; LIM; 2.
 DR PROSITE; PS00478; LIM DOMAIN 1; 2.
 DR PROSITE; PS00023; LIM DOMAIN 2; 2.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;
 KW Repeat; LIM domain; Metal-binding; Zinc.
 FT DOMAIN 148 200 LIM 1.
 FT DOMAIN 210 263 LIM 2.
 FT DNA BIND 367 426 HOMEBOX
 SQ SEQUENCE 469 AA; 52053 MW; FA9B43B8C7B9B22D CRC64;

Query Match 46.7%; Score 43; DB 1; Length 469;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKCYTCCKEPM 11
 ||| ||| ||| :
 Db 173 LQCYACROPL 182

RESULT 15
 EDHB METTF
 ID FDHB METTF STANDARD; PRT; 394 AA.
 AC Q50570;

```

DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Formate dehydrogenase beta chain (EC 1.2.1.2).
GN FDHB.
OS Methanobacterium thermoformicicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 3720 / Z-245;
RX MEDLINE=97158688; PubMed=9006048;
RA Noelling J., Reeve J.N.;
RT "Growth- and substrate-dependent transcription of the formate
dehydrogenase (fdhCAB) operon in Methanobacterium thermoformicum Z-
245."
RL J. Bacteriol. 179:899-908(1997).
CC -!- FUNCTION: M.THERMOFORMICICUM USE THE FDH ENZYME TO GROW ON
FORMATE.
CC -!- CATALYTIC ACTIVITY: Formate + NAD(+) = CO(2) + NADH.
CC -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (PROBABLE).
CC -!- SUBUNIT: Dimer of alpha and beta chains.
CC -!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
CC -!- SIMILARITY: STRONG, TO THE BETA SUBUNIT OF M.THERMOAUTOTROPHICUM
FDH.
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or send an email to license@isb-sib.ch).
-----
CC EMBL; U52681; AAC44821.1; -.
CC HSP; Q45560; LBWE.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; fer4; 1.
DR Pfam; PF04432; FthB_FdhB_C; 1.
DR Pfam; PF04432; FthB_FdhB_N; 1.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 2.
KW Oxidoreductase; NAD; Electron transport; Iron-sulfur; 4Fe-4S.
FT METAL 295 295 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 298 298 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 301 301 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 305 305 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 346 346 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 349 349 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 352 352 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 356 356 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 394 AA; 43683 MW; F95B3E85B4C44316 CRC64;
Query Match 45.7%; Score 42; DB 1; Length 394;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 2 LKCYTCKEPMTSAAC 16
Db 296 IKCYSCREACPICYC 310

```

Search completed: October 9, 2003, 14:10:10
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:07:37 ; Search time 39 Seconds
(without alignments)
39.454 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 ELKCYCKEPTMSAAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	91.3	103	2 A59031	ARS component B 81
2	58	63.0	15	2 A58945	anti-neoplastic ur
3	46	50.0	225	2 A69305	conserved hypothet
4	45	48.9	153	2 S36503	E6 protein - human
5	45	48.9	157	2 P69368	Carbon monoxide de
6	44	47.8	126	2 S53340	CD59 protein - rat
7	44	47.8	134	2 D45835	Ly6 homolog RK3 pr
8	44	47.8	224	2 S65960	mauM protein precu
9	44	47.8	388	2 T43019	probable DNA-bind
10	44	47.8	391	2 E83840	hypothetical prote
11	44	47.8	580	2 S13328	hypothetical prote
12	43	46.7	61	1 SMH01A	metallothionein IA
13	43	46.7	114	2 AF2315	hypothetical prote
14	43	46.7	154	2 S36527	E6 protein - human
15	43	46.7	155	1 W6WL56	E6 protein - human
16	43	46.7	295	2 G65018	ethanolamine ammon
17	43	46.7	295	2 G91042	ethanolamine ammon
18	43	46.7	295	2 B85887	ethanolamine ammon
19	43	46.7	365	2 C34895	SS RNA-binding pro
20	43	46.7	365	2 A34895	SS RNA-binding pro
21	43	46.7	469	1 JH0718	homeotic protein a
22	43	46.7	1322	2 T15689	hypothetical prote
23	42	45.7	71	2 B69428	hypothetical prote
24	42	45.7	572	2 G02845	zyxin - human
25	42	45.7	761	2 T33816	hypothetical prote
26	42	45.7	803	2 S45916	hypothetical prote
27	41	44.6	32	2 S19906	E6-II protein - hu
28	41	44.6	35	2 S19909	E6-III protein - h
29	41	44.6	47	2 S21825	E6-I protein - hum

CD59 protein - bab
E6 protein - human
hypothetical 22.8K
R01H10.4 protein (R01H10.4 protein (hypothetical prote
formate dehydrogen
hypothetical prote
hypothetical prote
hypothetical prote
retinoblastoma bin
proliferation pote
hemocytin - silkw
hypothetical prote
metallothionein II
metallothionein IR
metallothionein II

ALIGNMENTS

RESULT 1

A59031

ARS component B 81/S protein precursor - human

N;Alternate names: secreted Ly-6/uPAR related protein 1; SLURP-1

C;Species: Homo sapiens (man)

C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 29-Oct-1999

C;Accession: A59031; A58842

R;Mastrangeli, R.

submitted to the EMBL Data Library, August 1996

A;Description: ARS gene, component B.

A;Reference number: A59031

A;Accession: A59031

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-103 <MAS>

A;Cross-references: GB:X99977; NID:gl536901; PID:gl536901; PID:c265523; PID:gl536902

A;Experimental source: placenta

R;Ademann, K.; Wattler, F.; Wattler, S.; Heine, G.; Meyer, M.; Forssmann, W.G.; Nehls,

submitted to the Protein Sequence Database, July 1998

A;Description: Secreted protein, related to Ly-6, uPAR, soluble CD59, and snake and fro

A;Reference number: A58842

A;Accession: A58842

A;Molecule type: protein

A;Residues: 23-103 <ADE>

C;Genetics:

A;Gene: ARS

A;Introns: 20/1; 60/1

C;Keywords: glycoprotein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-22/Domain: propeptide #status predicted <PRO>

F;23-103/Product: ARS component B 81/S protein #status experimental <MAT>

F;25-50,28-37,94-99/Disulfide bonds: #status experimental

F;43-77,73-93/Disulfide bonds: (or 43-73, 77-93) #status experimental

F;64/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 91.3%; Score 84; DB 2; Length 103;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKCYCKEPTMSAAC 16

|||||

Db 23 LKCYCKEPTMSASC 37

RESULT 2

A58945

anti-neoplastic urinary protein - human (fragment)

N;Alternate names: ANUP

C;Species: Homo sapiens (man)

C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Apr-1999

C;Accession: A58945

R;Ridge, R.J.; Sloane, N.H.

Cytokine 8, 1-5, 1996
A:Title: Partial N-terminal amino acid sequence of the anti-neoplastic urinary protein
ytes.

A:Reference number: A58945; MUID:96351837; PMID:8742060

A:Accession: A58945

A:Molecule type: protein

A:Residues: 1-15 <RID>

A:Note: 13-Thr was also seen; residues 4 and 7 are assumed to be Cys; the authors report
ino terminal is blocked

C:Keywords: cytokine; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

Query Match 63.0%; Score 58; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 0.021;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELKCYTCCKEPTMSAA 15

Db 1 QLKXYYTXKEPTMSAA 15

RESULT 3

A69305

conserved hypothetical protein AF0441 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: A69305

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: A69305

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-225 <KLE>

A:Cross-references: GB:AE001074; GB:AE000782; NID:g2689397; PIDN:AAB90793.1; PID:g265018

Query Match 50.0%; Score 46; DB 2; Length 225;

Best Local Similarity 53.3%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 LKCYTCCKEPTMSAAC 16

Db 33 LNCYCYCDTPKTSNC 47

RESULT 4

S36503

E6 protein - human papillomavirus type 30

C:Species: human papillomavirus type 30

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S36503

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36503

A:Molecule type: DNA

A:Residues: 1-153

A:Cross-references: EMBL:X74474; NID:g396973; PIDN:CAA52543.1; PID:g396974

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 48.9%; Score 45; DB 2; Length 153;

Best Local Similarity 45.5%; Pred. No. 11;

Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKCYTCCKEPTMT 12

Db 2 LKCYTCCKEPTMT 12

Db 104 IRCYRCQOPLT 114

RESULT 5

F69368

carbon monoxide dehydrogenase, iron sulfur subunit (coof) homolog - Archaeoglobus fulg

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999

C:Accession: F69368

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: F69368

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-157 <KLE>

A:Cross-references: GB:AE001038; GB:AE000782; NID:g2689361; PIDN:AAB90290.1; PID:g2649

C:Superfamily: nrfC protein; ferredoxin 2[4Fe-4S] homology

F:92-152/Domain: ferredoxin 2[4Fe-4S] homology <FER1>

Query Match 48.9%; Score 45; DB 2; Length 157;

Best Local Similarity 53.3%; Pred. No. 11;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKCYTCCKEPTMSAAC 16

Db 66 LQCRHCEEPKCVAAAC 80

RESULT 6

S53340

CD59 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 28-May-1999

C:Accession: S53340; S53339

R:Rushmere, N.K.; Harrison, R.A.; van den Berg, C.W.; Morgan, B.P.

Biochem. J. 304, 595-601, 1994

A:Title: Molecular cloning of the rat analogue of human CD59: structural comparison wit

A:Reference number: S53339; MUID:95091697; PMID:7528012

A:Accession: S53340

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-126 <RUS>

A:Cross-references: GB:U48255; NID:g1199654; PIDN:AAA88909.1; PID:g1199655

A:Accession: S53339

A:Status: preliminary

A:Molecule type: protein

A:Residues: 23-24, 'X', 26-27, 'X', 29-34, 'X', 36-37, 'X', 39-40, 'X', 42-47, 'X', 49-58, 'X', 60, 'X'

C:Superfamily: Ly-6 antigen; Ly-6 homology

F:23-101/Domain: Ly-6 homology <LY6>

Query Match 47.8%; Score 44; DB 2; Length 126;

Best Local Similarity 50.0%; Pred. No. 14;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKCYTCCKEPTMS 13

Db 23 LRCYNCCLDPVSS 34

RESULT 7

D45835

Ly6 homolog RK3 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 31-Jan-2000

C:Accession: D45835; C45835

R:Friedman, S.; Palfrey, R.G.E.; Sirlin, S.; Haemmerling, U.

Immunogenetics 31, 104-111, 1990

A;Title: Analysis of three distinct Ly6-A-related cDNA sequences isolated from rat kidney
A;Reference number: A45835; MUID:90152758; PMID:2154400
A;Accession: D45835
A;Molecule type: mRNA
A;Residues: 1-134 <FRI>
A;Cross-references: GB:M30690; NID:g205249; PIDN:AAA41547.1; PID:g205250
A;Experimental source: clone RK3
A;Accession: C45835
A;Molecule type: mRNA
A;Residues: 2-134 <PR2>
A;Cross-references: GB:M30691; NID:g205251; PIDN:AAA41548.1; PID:g205252
A;Experimental source: clone RK11
C;Superfamily: Ly-6 antigen; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linked
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-105/Product: Ly6 homolog RK3 #status predicted <MAT>
F;106-134/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;105/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)

Query Match 47.8%; Score 44; DB 2; Length 134;
Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAAC 16
|||||:|:|:|
Db 27 LKCYSCIEVPLNANC 41

RESULT 8
S65960
mauM protein precursor - Paracoccus denitrificans
C;Species: Paracoccus denitrificans
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C;Accession: S65960
R;van der Palen, C.J.N.M.; Slotboom, D.J.; Jongejan, L.; Reijnders, W.N.M.; Harms, N.; D
Eur. J. Biochem. 230, 860-871, 1995
A;Title: Mutational analysis of mau genes involved in methylamine metabolism in Paracoc
A;Reference number: S65958; MUID:95324575; PMID:7601147
A;Accession: S65960
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-224 <VAN>
A;Cross-references: EMBL:U15028; NID:g595839; PIDN:AAA86468.1; PID:g595842
C;Genetics:
A;Gene: mauM

C;Superfamily: conserved hypothetical protein H10345; ferredoxin 2[4Fe-4S] homology
F;1-46/Domain: signal sequence #status predicted <SIG>
F;47-224/Product: mauM protein #status predicted <MAT>
F;57-122/Domain: ferredoxin 2[4Fe-4S] homology <FER6>

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Best Local Similarity 43.8%; Pred. No. 21;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELKCYTCKEPMTSAAC 16
|:|:|:|:|:|:|
Db 99 EVPCYMKDVPFCARAC 114

RESULT 9
T43019
probable DNA-binding protein - African malaria mosquito retrotransposon Q retrotranspos
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43019
R;Besanaky, N.J.; Bedell, J.A.; Mukabayire, O.
Insect Mol. Biol. 3, 49-56, 1994
A;Title: Q: a new retrotransposon from the mosquito Anopheles gambiae.
A;Reference number: Z22286; MUID:94348637; PMID:8069416
A;Accession: T43019
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-388 <BES>

A;Cross-references: EMBL:U03849; NID:g432429; PID:g577351; PIDN:AAAS3488.1
A;Experimental source: strain G3; clone Q-22
C;Genetics:
A;Mobile element: retrotransposon Q

Query Match 47.8%; Score 44; DB 2; Length 388;
Best Local Similarity 38.5%; Pred. No. 33;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPMTSAAC 16
|:|:|:|:|:|
Db 16 CFSCAEPLEATGC 28

RESULT 10
E83840
hypothetical protein BH1525 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E83840
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hi
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E83840
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-391 <STO>
A;Cross-references: GB:AP001512; GB:BA000004; NID:gl0174030; PIDN:BA05244.1; GSPDB:GNO
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1525

Query Match 47.8%; Score 44; DB 2; Length 391;
Best Local Similarity 43.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELKCYTCKEPMTSAAC 16
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Db 267 ETTCAQCRTPMKGSAC 282

RESULT 11
S13328
hypothetical protein 1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Feb-1997
C;Accession: S13328
R;O'Hare, K.; Alley, M.R.K.; Cullingford, T.E.; Driver, A.; Sanderson, M.J.
Mol. Gen. Genet. 225, 17-24, 1991
A;Title: DNA sequence of the Doc retroposon in the white-one mutant of Drosophila melan
A;Reference number: S13328; MUID:91155930; PMID:1705654
A;Accession: S13328
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-580 <MOL>
A;Cross-references: EMBL:X17551
C;Genetics:
A;Gene: FlyBase:Doc
A;Cross-references: FlyBase:FBgn0000481

Query Match 47.8%; Score 44; DB 2; Length 580;
Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 CYTCKEPMTSAAC 16
|:|:|:|:|:|
Db 418 CVVCSEPTTANC 430

RESULT 12
SMH01A
metallothionein 1A - human

C:Species: Homo sapiens (man)
 C:Date: 24-Jun-1987 #sequence_revision 09-Sep-1994 #text_change 22-Jun-1999
 C:Accession: A24502
 R:Richards, R.I.; Heguy, A.; Karin, M.
 Cell 37, 263-272, 1984
 A:Title: Structural and functional analysis of the human metallothionein-IA gene: differed
 A:Reference number: A24502; PMID:84205649; PMID:6327055
 A:Accession: A24502
 A:Molecule type: DNA
 A:Residues: 1-61 <RIC>
 A:Cross-references: GB:K01383; NID:gl87536; PIDN:AAA59586.1; PID:g386864
 C:Genetics:
 A:Gene: GDB:MT1A; MT1
 A:Cross-references: GDB:125559; OMIM:156350
 A:Map position: 16q13-16q13
 A:Introns: 10/1; 32/1
 C:Superfamily: metallothionein
 F:1-29/Domain: beta <NH2>
 F:30-61/Domain: alpha <AUP>
 F:1/Modified site: acetylated amino end (Met) #status predicted
 F:5,7,13,15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted
 F:33,34,36,37,41,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status pre

Query Match 46.7%; Score 43; DB 1; Length 61;
 Best Local Similarity 40.9%; Pred. No. 11;
 Matches 9; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

QY 1 ELKCVTCKE-----PMTSAAC 16
 DB 23 ECKNSCKKSCCSCCPMSCAKC 44

RESULT 13
 AF2315
 hypothetical protein alr4077 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120 [imported]
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AF2315
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; PMID:21595285; PMID:11759840
 A:Accession: AF2315
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA875776.1; PID:gl17133212; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr4077

Query Match 46.7%; Score 43; DB 2; Length 114;
 Best Local Similarity 58.3%; Pred. No. 18;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CYTCKEPMTSAA 15
 DB 36 CYTCGQDQNSAS 47

RESULT 14
 S36527
 B6 protein - human papillomavirus type 53
 C:Species: human papillomavirus type 53
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S36527
 R:Deilius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469

A:Accession: S36527
 A:Molecule type: DNA
 A:Residues: 1-154
 A:Cross-references: EMBL:X74482; NID:g397046; PIDN:CAA52591.1; PID:g397047
 C:Superfamily: papillomavirus E6 protein
 C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 46.7%; Score 43; DB 2; Length 154;
 Best Local Similarity 45.5%; Pred. No. 22;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMT 12
 DB 105 IRCVRCQHPLT 115

RESULT 15
 W6WL56
 B6 protein - human papillomavirus type 56
 C:Species: human papillomavirus type 56
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
 C:Accession: A33377; S36579
 R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.
 J. Gen. Virol. 70, 3099-3104, 1989
 A:Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
 A:Reference number: A33377; PMID:90063558; PMID:2555440
 A:Accession: A33377
 A:Molecule type: DNA
 A:Residues: 1-155 <LOE>
 R:Deilius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A:Description: Primer-directed sequencing of human papillomavirus types.
 A:Reference number: S36469
 A:Accession: S36579
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-155 <DBL>
 A:Cross-references: EMBL:X74483; NID:g397053; PIDN:CAA52596.1; PID:g397054
 C:Superfamily: papillomavirus E6 protein
 C:Keywords: DNA binding; early protein; transforming protein; zinc finger
 F:33-69/Region: zinc finger CCCC motif
 F:106-142/Region: zinc finger CCCC motif

Query Match 46.7%; Score 43; DB 1; Length 155;
 Best Local Similarity 45.5%; Pred. No. 22;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMT 12
 DB 104 IRCVRCQSPLT 114

Search completed: October 9, 2003, 14:12:39
 Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:09:47 ; Search time 26 Seconds
(without alignments)
99.156 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 LKCYCKEPMPTSAAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	94.6	16	8	US-08-986-606C-1
2	58	63.0	558	9	US-09-864-761-47724
3	50	54.3	212	15	US-10-091-458-49
4	50	54.3	272	15	US-10-091-458-36
5	50	54.3	612	12	US-10-114-133-90
6	48	52.2	270	10	US-09-764-864-1433
7	48	52.2	293	9	US-09-925-301-1119
8	46	50.0	125	10	US-09-978-295A-454
9	46	50.0	125	10	US-09-978-697-454
10	46	50.0	125	10	US-09-978-192A-454
11	46	50.0	125	10	US-09-999-832A-454
12	46	50.0	125	11	US-09-978-189-454
13	46	50.0	125	11	US-09-978-608A-454
14	46	50.0	125	11	US-09-978-585A-454
15	46	50.0	125	11	US-09-978-191A-454

16	46	50.0	125	11	US-09-978-403A-454	Sequence 454, App
17	46	50.0	125	11	US-09-978-564A-454	Sequence 454, App
18	46	50.0	125	11	US-09-999-833A-454	Sequence 454, App
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34	46	50.0	125	12	US-10-143-030A-454	Sequence 454, App
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36	46	50.0	125	12	US-10-145-128A-454	Sequence 454, App
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40	46	50.0	125	12	US-10-145-089A-454	Sequence 454, App
41	46	50.0	125	12	US-10-013-926A-454	Sequence 454, App
42	46	50.0	125	12	US-10-145-017A-454	Sequence 454, App
43	46	50.0	125	12	US-10-164-728A-454	Sequence 454, App
44	46	50.0	125	12	US-10-165-067A-454	Sequence 454, App
45	46	50.0	125	12	US-10-218-765-140	Sequence 140, App

ALIGNMENTS

RESULT 1
US-08-986-606C-1
; Sequence 1, Application US/08986606C
; Publication No. US20020061851A1
; GENERAL INFORMATION:
; APPLICANT: Sloane, Nathan H
; TITLE OF INVENTION: Sixteen Amino Acid of the Antineoplastic Protein (ANUP)
; TITLE OF INVENTION: as a Pharmaceutically Active Anti-Tumor Agent
; FILE REFERENCE: 99181
; CURRENT APPLICATION NUMBER: US/08/986,606C
; CURRENT FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; LOCATION: 1
; OTHER INFORMATION: Xaa is -N-Terminal pyrroglutamyl (pyroGLU)
; OTHER INFORMATION: Description of Artificial Sequence, the partial N-terminal
; OTHER INFORMATION: amino acid sequence of the Antineoplastic Protein (ANUP)
US-08-986-606C-1

Query Match 94.6%; Score 87; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKCYCKEPMPTSAAC 16
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Db 2 LKCYCKEPMPTSAAC 16
|||||

RESULT 2
US-09-864-761-47724
; Sequence 47724, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

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; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47724
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
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; OTHER INFORMATION: MAP TO AC011451.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
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; US-09-864-761-47724
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Db 285 KVCYCKGKPTSSAC 298
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US-10-091-458-49
; Sequence 49, Application US/10091458
; Publication No. US20030068627A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT206C1
; CURRENT APPLICATION NUMBER: US/10/091,458
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,900
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
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; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
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; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
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; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
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; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
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; PRIOR FILING DATE: 2000-10-20
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; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
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; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
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; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
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Query Match 54.3%; Score 50; DB 15; Length 212;
Best Local Similarity 53.8%; Pred. No. 4.3;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPTMTSAAC 16
|:|:|:|:|:|:|
Db 172 CFTCQETPTSTGC 184

RESULT 4
US-10-091-458-36
; Sequence 36, Application US/10091458
; Publication No. US20030068627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ06C1
; CURRENT APPLICATION NUMBER: US/10/091,458
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,900
; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
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; PRIOR FILING DATE: 2000-09-08

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Query Match      54.3%; Score 50; DB 15; Length 272;
Best Local Similarity 53.8%; Pred. No. 5.5;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY      4  CVTCKEPMTSAC 16
Db      172  CFTCQEPFSTGC 184

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RESULT 5
US-10-114-153-90
; Sequence 90, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Caeman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha

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; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC AC
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
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; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 90
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-90

Query Match      54.3%; Score 50; DB 12; Length 612;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4  CVTCKEPMTSAC 16
Db      547  CFTCQEPFSTGC 559

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RESULT 6
US-09-764-864-1433
; Sequence 1433, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1433
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-764-864-1433

Query Match 52.2%; Score 48; DB 10; Length 270;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CYTCKPMTSA 14
 | | | | |
 Db 199 CTTCKQPPTSA 209

RESULT 7

US-09-925-301-1119
 ; Sequence 1119, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PAL06
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1119
 ; LENGTH: 293
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (170)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-301-1119

Query Match 52.2%; Score 48; DB 9; Length 293;
 Best Local Similarity 72.7%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CYTCKPMTSA 14
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 Db 199 CTTCKQPPTSA 209

RESULT 8

US-09-978-295A-454
 ; Sequence 454, Application US/09978295A
 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 50.0%; Score 46; DB 10; Length 125;
 Best Local Similarity 42.9%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 2 LKCYTCPE-----MTSAC 16
 Db 23 LKCYTCPEPTGVSDCVTIATC 43

RESULT 9

US-09-978-697-454
 ; Sequence 454, Application US/09978697
 ; Patent No. US20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same

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; FILE REFERENCE: P2630PIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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Query Match 50.0%; Score 46; DB 10; Length 125;

Best Local Similarity 42.9%; Pred. No. 10;

Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 2 LKCYCKEP-----MTSAC 16
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 Db 23 LRCYVCPEPTGVSDCVTIATC 43

RESULT 10

US-09-978-192A-454
 ; Sequence 454, Application US/09978192A
 ; Patent No. US20020177553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C9
 ; CURRENT APPLICATION NUMBER: US/09/978,192A
 ; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 50.0%; Score 46; DB 10; Length 125;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 2 LKCYTKCP-----MTSAAAC 16
Db 23 LRCYVCPPTGVSDCVTIATC 43

RESULT 11

US-09-999-832A-454
; Sequence 454, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P26301C63
; CURRENT APPLICATION NUMBER: US/09/999, 832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15
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Query Match          50.0%; Score 46; DB 10; Length 125;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy  2 LKVCYCKEP-----MTSAAC 16
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Db  23 LRCVCEPTGVSDCVTIATC 43

RESULT 12
US-09-978-189-454
; Sequence 454, Application US/09978189
; Publication No. US20030004102A1
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; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/079923
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704

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; PRIOR APPLICATION NUMBER: 60/085697

Query Match          50.0%; Score 4
Best Local Similarity 42.9%; Pred. N
Matches          9; Conservative      2; Mismatches 2

QY 2 LKCYTCKEP-----MTSAAC 16
DB 23 LRCYVCPEPTGVSDCVTIATC 43

RESULT 13
US-09-978-608A-454
; Sequence 454, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transferred
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978-608A
; CURRENT FILING DATE: 2004-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior application removed - See File Wrapper
; SEQ ID NO 454
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-454

Query Match          50.0%; Score 4
Best Local Similarity 42.9%; Pred. N
Matches          9; Conservative      2; Mismatches 2

QY 2 LKCYTCKEP-----MTSAAC 16
DB 23 LRCYVCPEPTGVSDCVTIATC 43

RESULT 14
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; Sequence 454, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/080334
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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C5
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 454
; LENGTH: 125
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; US-09-978-585A-454

Query Match 50.0%; Score 46; DB 11; Length 125;
Best Local Similarity 42.9%; Pred. NO. 10;
Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 2 LKCVTKCEP-----MTSAAC 16
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US-09-978-191A-454
; Sequence 454, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
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, PRIOR APPLICATION NUMBER: 60/085704
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085697

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Query Match 50.0%; Score 46; DB 11; Length 125;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 4; Indels

Search completed: October 9, 2003, 14:13:48
Job time : 27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 14:08:17 ; Search time 29 Seconds
(without alignments)
23.344 Million cell updates/sec

Title: US-08-986-606E-1
Perfect score: 92
Sequence: 1 ELKCYTCKEPMTSAAAC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	41	44.6	355	4	US-09-252-991A-21002
6	41	44.6	409	4	US-09-724-864-53
7	41	44.6	1404	4	US-08-801-308-1
8	40	43.5	61	2	US-08-785-530-6
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33	40	43.5	1384	3	US-08-976-255-11	Sequence 11, Appli
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45	38	41.3	106	3	US-09-383-586-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-08-448-561-1
; Sequence 1, Application US/08448561
; Patent No. 5908827
; GENERAL INFORMATION:
; APPLICANT: SIRNA, Antonio
; TITLE OF INVENTION: NEW PROTEIN FROM URINE NAMED COMPONENT B
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,561
; FILING DATE: 22-JAN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT RM 92 A/919
; FILING DATE: 22-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SIRNA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: URINE
; US-08-448-561-1

Query Match 91.3%; Score 84; DB 2; Length 81;
Best Local Similarity 93.3%; Pred. No. 3.9e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-252-991A-21002
; Sequence 21002, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21002
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21002

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RESULT 7
US-08-801-308-1
; Sequence 1, Application US/09801308
; Patent No. 6368790
; GENERAL INFORMATION:
; APPLICANT: SCOTT, Robert E.
; TITLE OF INVENTION: CDNA ENCODING P2P PROTEINS AND USE OF
; TITLE OF INVENTION: P2P CDNA-DERIVED ANTIBODIES AND ANTISENSE REAGENTS IN
; TITLE OF INVENTION: DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL,
; TITLE OF INVENTION: ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Weiser & Associates, P.C.
; STREET: 230 S. Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,308
; FILING DATE: 18-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 372.6435P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383

RESULT 9
US-09-123-850-6
; Sequence 6, Application US/09123850
; Patent No. 5955428
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09123,850
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,530
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0194 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 305363
US-09-123-850-6
Query Match 43.5%; Score 40; DB 2; Length 61;
Best Local Similarity 40.9%; Pred. No. 17;
Matches 9; Conservative 2; Mismatches 5; Indels 5; Gaps 1;
Qy 1 ELKCYTKCE-----PMTSAAC 16
Db 23 ECKCTTKKSCSCCPVCAK 44
RESULT 10
US-08-675-508-2
; Sequence 2, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0066 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: SCARH-2
CLONE:
US-08-675-508-2
Query Match 43.5%; Score 40; DB 2; Length 123;
Best Local Similarity 40.0%; Pred. No. 34;
Matches 6; Conservative 4; Mismatches 5; Indels 5; Gaps 0;
Qy 2 LKCYTCKEPMTSAAC 16
Db 21 LLCYSCKAQVSNEDC 35
RESULT 11
US-09-203-939-2
; Sequence 2, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
; NAME/KEY: SITE
; LOCATION: (71)..(82)
; NAME/KEY: SITE
; LOCATION: (67)..(81)
US-09-203-939-2
Query Match 43.5%; Score 40; DB 3; Length 123;
Best Local Similarity 40.0%; Pred. No. 34;
Matches 6; Conservative 4; Mismatches 5; Indels 5; Gaps 0;

QY 2 LKCYCTCKEPMNTSAAC 16
 | | | | | : : : |
 Db 21 LLCYSCKAQVSNEDC 35

RESULT 12
 US-09-203-939-4
 ; Sequence 4, Application US/09203939
 ; Patent No. 6258939
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US11
 ; CURRENT APPLICATION NUMBER: US/09/203,939
 ; CURRENT FILING DATE: 2000-12-02
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: MURINE PSCA (mpSCA)
 US-09-203-939-4

Query Match 43.5%; Score 40; DB 3; Length 123;
 Best Local Similarity 40.0%; Pred. No. 34;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKCYCTCKEPMNTSAAC 16
 | | | | | : : : |
 Db 21 LQCYCTAQMNDRDC 35

RESULT 13
 US-09-203-939-6
 ; Sequence 6, Application US/09203939
 ; Patent No. 6258939
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US11
 ; CURRENT APPLICATION NUMBER: US/09/203,939
 ; CURRENT FILING DATE: 2000-12-02
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: HUMAN PSCA (hpSCA)
 US-09-203-939-6

Query Match 43.5%; Score 40; DB 3; Length 123;
 Best Local Similarity 40.0%; Pred. No. 34;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKCYCTCKEPMNTSAAC 16

Db 21 LLCYSCKAQVSNEDC 35
 | | | | | : : : |

RESULT 14
 US-09-203-939-7
 ; Sequence 7, Application US/09203939
 ; Patent No. 6258939
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US11
 ; CURRENT APPLICATION NUMBER: US/09/203,939
 ; CURRENT FILING DATE: 2000-12-02
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: MURINE PSCA (mpSCA)
 US-09-203-939-7

Query Match 43.5%; Score 40; DB 3; Length 123;
 Best Local Similarity 40.0%; Pred. No. 34;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKCYCTCKEPMNTSAAC 16
 | | | | | : : : |
 Db 21 LQCYCTAQMNDRDC 35

RESULT 15
 US-09-251-835-2
 ; Sequence 2, Application US/09251835A
 ; Patent No. 6261789
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
 ; FILE REFERENCE: 30435.54US12
 ; CURRENT APPLICATION NUMBER: US/09/251,835A
 ; CURRENT FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: HUMAN PSCA (hpSCA)
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (50)...(64)
 ; NAME/KEY: SITE
 ; LOCATION: (71)...(82)
 ; NAME/KEY: SITE

; LOCATION: (67)..(81)
US-09-251-835-2

Query Match 43.5%; Score 40; DB 3; Length 123;
Best Local Similarity 40.0%; Pred. No. 34;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAC 16
Db 21 LLCYSCKAQVSNEDC 35

Search completed: October 9, 2003, 14:13:14
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:03:46 ; Search time 83 Seconds
(without alignments)
30.598 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 ELKCYTCKEPTMSAAC 16

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	16	23	ABB83280
2	84	91.3	81	20	AAW94613
3	84	91.3	103	15	AAW70984
4	84	91.3	103	21	AAW24039
5	79	85.9	15	21	AAW03300
6	78	84.8	14	15	AAW03299
7	75	81.5	14	15	AAW03298
8	58	63.0	558	22	ABB37697
9	58	63.0	739	22	ABG03917
					N-terminal peptide
					Human LUS-1 protei
					Component B protei
					Human PRO2038 prot
					Antineoplastic uri
					Antineoplastic uri
					Antineoplastic uri
					Peptide #5203 enco
					Novel human diagno

10	52	56.5	2931	22	ABB68229	Drosophila melanog
11	50	54.3	212	22	AAW99933	Human polypeptide
12	50	54.3	272	22	AAW99920	Human polypeptide
13	50	54.3	514	24	ABU11798	Human MDDT polypep
14	50	54.3	612	24	ABU12085	Human NOV26a CG938
15	48	52.2	240	23	AAW66137	Human MPO-110 poly
16	48	52.2	270	22	AAU16480	Human novel secret
17	48	52.2	270	24	ABU55549	Human novel polype
18	48	52.2	293	21	AAW43674	Human cancer assoc
19	48	52.2	773	23	AAW66135	Human MPO-110 poly
20	48	52.2	773	23	AAW66136	Human MPO-110 poly
21	48	52.2	835	24	ABU56447	Lung cancer-associ
22	47	51.1	55	22	AAW49256	Ap LIM domain 1.
23	47	51.1	132	23	AAU09169	Human heat shock p
24	47	51.1	320	22	AAU04898	Micromonospora eve
25	46	50.0	84	22	AAE03360	Human gene 10 enco
26	46	50.0	125	20	AAW41756	Human PRO788 prote
27	46	50.0	125	21	AAW44312	Human PRO788 (ONQ4
28	46	50.0	125	21	AAW33439	Human PRO788 prote
29	46	50.0	125	21	AAW24415	Human growth facto
30	46	50.0	125	21	AAW03000	Human gene 10 enco
31	46	50.0	125	22	AAE03301	Human gene 10 enco
32	46	50.0	125	22	AAE03327	Human PRO788 prote
33	46	50.0	125	22	AAW50915	Human PRO788 prote
34	46	50.0	125	23	ABG64428	Human albumin fusi
35	46	50.0	125	23	ABG64430	Human albumin fusi
36	46	50.0	125	23	ABW95477	Human angiotensin
37	46	50.0	125	23	ABB84871	Human PRO788 prote
38	46	50.0	125	23	AAU83661	Human PRO788 prote
39	46	50.0	125	24	ABU61142	Human PRO788 polyp
40	44	47.8	79	20	AAW27322	Rat CDS9 protein f
41	44	47.8	136	23	AAE14727	Human Alzheimer's
42	44	47.8	214	19	AAW98557	H. pylori GHPO 168
43	43	46.7	148	22	ABW67787	Drosophila melanog
44	43	46.7	155	22	AAW98452	Human papillomavir
45	43	46.7	469	22	ABB58444	Drosophila melanog

ALIGNMENTS

RESULT 1

ABB83280

1. ABB83280 standard; peptide; 16 AA.

XX ABB83280;

XX AC

XX 29-AUG-2002 (first entry)

XX N-terminal peptide fragment of Antineoplastic protein, ANUP.

XX Antineoplastic protein; ANUP; cytostatic; antitumour; apoptosis; tumour.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "Pyroglutamic acid"

XX US2002061851-A1.

XX 23-MAY-2002.

XX 08-DEC-1997; 97US-0986606.

XX 08-DEC-1997; 97US-0986606.

XX (SLAO/) SLAONE N H.

XX Slaone NH;

XX WPI; 2002-489588/52.

XX

PT Use of partial N-terminal hexadeca peptide of antineoplastic protein to
 PT kill human tumor cells using human breast tumor cell line as model -
 XX
 PS Claim 2; Page 2; 3pp; English.
 XX
 CC The present sequence is an N-terminal peptide fragment of the
 CC Antineoplastic protein (ANUP). This peptide is a pharmacologically active
 CC antitumor agent, and has approx. 50% of the ANUP protein's anti-tumour
 CC activity with only 10% of the molecular weight. This peptide is claimed
 CC to exert its action by killing tumour cells (apoptosis). Antitumour
 CC activity is only achieved in the presence of sodium dodecyl sulphate
 CC (SDS).
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 92; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELKCYTCCKEPTMSAAC 16
 DB 1 ELKCYTCCKEPTMSAAC 16
 RESULT 2
 AAW94613
 ID AAW94613 standard; protein; 81 AA.
 XX
 AC AAW94613;
 XX
 XX 28-APR-1999 (first entry)
 DT
 XX Human LUS-I protein.
 DE
 XX Human; LUS-I; infection; cancer; autoimmune disease; oedema; asthma;
 KW paroxysmal nocturnal haemoglobinuria; diagnosis.
 KW
 OS Homo sapiens.
 XX
 XX WO9856810-A2.
 PN
 XX 17-DEC-1998.
 PD
 XX 09-JUN-1998; 98WO-EP03460.
 PF
 XX 06-NOV-1997; 97DE-1049073.
 PR
 XX 09-JUN-1997; 97DE-1024301.
 XX
 XX (FORS/) FORSMANN W.
 PA
 XX Adermann K, Bensch K, Forssmann W, Heine G, Meyer M;
 PI Nehls M, Schulz-Knappe P;
 PI
 XX WPI; 1999-080884/07.
 XX
 XX New protein, LUS-I, and related nucleic acid, antibodies, inhibitors
 PT and transgenic animals - for treatment and diagnosis of infections,
 PT cancer, autoimmune disease, oedema, asthma and paroxysmal nocturnal
 PT haemoglobinuria
 XX
 XX Claim 1; Page 9; 12pp; German.
 XX
 CC The present sequence represents a human protein designated LUS-I.
 CC The present invention also describes its cyclic, glycosylated,
 CC phosphorylated, acetylated, amidated or side chain-coupled derivatives
 CC and biologically active fragments. The LUS-I protein, nucleotide
 CC sequence and antibodies can be used for diagnosis and treatment of
 CC bacterial and viral infections; under- or over-expression of LUS-I;
 CC cancer (of the cervix uteri; small cell bronchial, pancreatic or mammary
 CC carcinomas, or melanoma); autoimmune diseases; angioneurotic oedema;
 CC bronchial asthma or paroxysmal nocturnal haemoglobinuria. LUS-I
 CC nucleotide sequences are also useful for treating (non-)somatic genetic
 CC disorders associated with inadequate or abnormal expression of LUS-I.

CC Transgenic animals are useful for studying effects of LUS-I on formation
 CC and development of tumours. Diagnostically, antibodies are used in
 CC standard immunoassays to detect the protein in tissues and body fluids,
 CC while analysis of the nucleotide sequence (particularly by amplification)
 CC is used to detect diseases that can be treated with the protein.
 XX
 XX Sequence 81 AA;
 SQ
 Query Match 91.3%; Score 84; DB 20; Length 81;
 Best Local Similarity 93.3%; Pred. No. 2.5e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LKCYTCCKEPTMSAAC 16
 DB 1 LKCYTCCKEPTMSAAC 15
 RESULT 3
 AAR70984
 ID AAR70984 standard; Protein; 103 AA.
 XX
 AC AAR70984;
 XX
 XX 25-MAR-2003 (updated)
 DT 27-JUL-1995 (first entry)
 XX
 XX Component B protein.
 DE
 XX Probe; component B; promoter; human; signal peptide; primer; RACE;
 KW low molecular weight protein; urine; TGF-alpha; receptor; amplify;
 KW inflammation; coagulation; tumour; angiogenesis.
 XX
 XX Homo sapiens.
 OS
 XX WO9414959-A1.
 PN
 XX 07-JUL-1994.
 PD
 XX 21-DEC-1993; 93WO-EP03645.
 PF
 XX 22-DEC-1992; 92IT-RM00919.
 PR
 XX (ISTF) ARS APPLIED RES SYST HOLDING NV.
 PA
 XX Sirna A;
 PI
 XX WPI; 1994-234696/28.
 DR
 XX N-PSDB; AAQ87876, AAQ87878.
 XX
 XX New protein, component B, isolated from urine - with
 PT antiinflammatory, anticoagulant and anti-tumour activities, also
 PT related nucleic acid, vectors and transformed cells.
 PT
 XX Claim 1; Fig 2; 55pp; English.
 XX
 CC This sequence represents the genomic sequence encoding component B.
 CC This sequence was isolated using the probes given in AAQ87854-69.
 CC The component B gene contains three exons and two introns.
 CC Exon 1 is 84 bp and contains 26 bases of untranslated mRNA. It
 CC encodes 19 amino acids of the putative signal peptide and is
 CC separated from exon 2 by an intron of 410 bp. Exon 2 is 120 bp and
 CC codes for 3 amino acids of the putative signal sequence and 37 amino
 CC acids of the mature protein. It is separated from exon 3 by an
 CC intron of about 550 bp. Exon 3 is 326 bp and encodes the C-terminal
 CC contains a poly-A signal 14 bp upstream of the 3' processing site.
 CC Component B is a low molecular weight protein which may be isolated
 CC from human urine by adsorption at acid pH on kaolin, then extraction
 CC with sodium hydroxide. It inhibits binding of TGF-alpha to its
 CC receptor, and so has antiinflammatory, anticoagulant and/or antitumour
 CC activities. It may also be used to treat conditions associated with
 CC altered levels of TGF-alpha, eg. behavioural or hormonal disturbances and
 CC angiogenesis.

CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 103 AA;

Query Match 91.3%; Score 84; DB 15; Length 103;
 Best Local Similarity 93.3%; Pred. No. 3.2e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKCYTCCKEPMNTSAAC 16
 |||||
 Db 23 LKCYTCCKEPMNTSASC 37

RESULT 4
 AAB24039
 ID AAB24039 standard; Protein; 103 AA.

XX
 AC AAB24039;

DT 25-JAN-2001 (first entry)

XX Human PRO2038 protein sequence SEQ ID NO:53.

DE Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumorigenesis; anticancer; detection.

XX Homo sapiens.

XX WO2000053750-A1.

XX 14-SEP-2000.

XX 02-DEC-1999; 99WO-US28551.

XX 08-MAR-1999; 99WO-US05028.

PR 01-SEP-1999; 99WO-US20111.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28634.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;

XX WPI; 2000-594320/56.

XX N-PSDB; AAC58121.

XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit

XX the growth of tumors in mammals; and to identify inhibitors of PRO

XX polypeptide activity or expression -

XX Claim 61; Fig 38; 226pp; English.

XX The present invention describes an antibody that binds to a human

XX protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;

XX PRO4344; PRO1297; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354;

XX PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has

XX anticancer activity and can be used to diagnose tumours in mammals, by

XX detecting complex formation when the antibody is contacted with test

XX cells. Increased expression of genes encoding (I) can also be detected

XX to diagnose tumours. Agents which inhibit the activity of (I),

XX especially the antibodies, or an antisense oligonucleotide which

XX hybridises to genes encoding (I), can be used to inhibit tumour growth,

XX preferably by inducing cell death. Methods from the present invention

CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 103 AA;

Query Match 91.3%; Score 84; DB 15; Length 103;
 Best Local Similarity 93.3%; Pred. No. 3.2e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKCYTCCKEPMNTSAAC 16
 |||||
 Db 23 LKCYTCCKEPMNTSASC 37

RESULT 4
 AAB24039
 ID AAB24039 standard; Protein; 103 AA.

XX
 AC AAB24039;

DT 25-JAN-2001 (first entry)

XX Human PRO2038 protein sequence SEQ ID NO:53.

DE Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumorigenesis; anticancer; detection.

XX Homo sapiens.

XX WO2000053750-A1.

XX 14-SEP-2000.

XX 02-DEC-1999; 99WO-US28551.

XX 08-MAR-1999; 99WO-US05028.

PR 01-SEP-1999; 99WO-US20111.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28634.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;

XX WPI; 2000-594320/56.

XX N-PSDB; AAC58121.

XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit

XX the growth of tumors in mammals; and to identify inhibitors of PRO

XX polypeptide activity or expression -

XX Claim 61; Fig 38; 226pp; English.

XX The present invention describes an antibody that binds to a human

XX protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;

XX PRO4344; PRO1297; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354;

XX PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has

XX anticancer activity and can be used to diagnose tumours in mammals, by

XX detecting complex formation when the antibody is contacted with test

XX cells. Increased expression of genes encoding (I) can also be detected

XX to diagnose tumours. Agents which inhibit the activity of (I),

XX especially the antibodies, or an antisense oligonucleotide which

XX hybridises to genes encoding (I), can be used to inhibit tumour growth,

XX preferably by inducing cell death. Methods from the present invention

CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 103 AA;

Query Match 91.3%; Score 84; DB 21; Length 103;
 Best Local Similarity 93.3%; Pred. No. 3.2e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKCYTCCKEPMNTSAAC 16
 |||||
 Db 23 LKCYTCCKEPMNTSASC 37

RESULT 5
 AAW03300
 ID AAW03300 standard; peptide; 15 AA.

XX
 AC AAW03300;

DT 22-DEC-1997 (first entry)

XX Antineoplastic urinary protein blocked N-terminal sequence.

XX ANUP; antineoplastic urinary protein; cytokine; anticancer.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "pyroglutamyl residue"

XX Misc-difference 13 /label= Ser, Thr

XX /note= "it is uncertain which of Ser and Thr is present in this position"

XX US5298604-A.

XX 29-MAR-1994.

XX 02-SEP-1993; 93US-0116539.

XX 27-JUL-1992; 92US-0919885.

XX 02-SEP-1993; 93US-0116539.

XX (SLOA/) SLOANE N H.

XX Sloane NH;

XX WPI; 1994-100399/12.

XX Partial free N-terminal sequence of antineoplastic urinary protein -

XX useful for cancer therapy

XX Disclosure; -; 4pp; English.

XX The invention relates to the elucidation of the partial N-terminal

XX amino acid sequence of antineoplastic urinary protein (ANUP). This

XX antitumour cytokine is present in human granulocytes and is excreted

XX from the serum into the urine. The protein contains a blocked N-terminal

XX amino acid, the blocking group of which has been identified as a

XX pyroglutamyl residue. The electrophoretically homogeneous ANUP (monomer

XX 16 kD) is treated with pyroglutamyl aminopeptidase to liberate the free

XX N-terminal amino group. The deblocked protein is transblotted and the

XX amino acid sequence of the electrophoretically homogeneous deblocked

XX protein is determined. It is found to be Leu-Lys-Cys-Tyr-Thr-Cys-Lys-

XX Glu-Pro-Met-Thr-(Thr or Ser)-Ala-Ala. ANUP may be utilised as a potential

XX antitumour chemotherapeutic agent to treat human neoplastic disease, as

XX it is non-toxic to human cells, specifically inhibits only human cancer

XX cell lines and causes regression of human tumour cell lines implanted in

XX nude mice.

XX The present sequence represents the pyroglutamyl-blocked N-terminal

XX sequence of ANUP, as deduced from its description in the patent.

XX Sequence 15 AA;

XX Query Match 85.9%; Score 79; DB 15; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.6e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELKCYTCKEPMTSAA 15
|||||

Db 1 ELKCYTCKEPMTXAA 15
|||||

RESULT 6

AAW03299
ID AAW03299 standard; peptide; 14 AA.

XX AC AAW03299;

XX DT 22-DEC-1997 (first entry)

XX DE Antineoplastic urinary protein deblocked N-terminal sequence.

XX KW ANUP; antineoplastic urinary protein; cytokine; anticancer.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 12

XX FT /note= "it is unsure whether this residue is Ser or
Thr (see also AAW03298 and AAW03300)"

XX PN US5298604-A.

XX PD 29-MAR-1994.

XX PF 02-SEP-1993; 93US-0116539.

XX PR 27-JUL-1992; 92US-0919885.

XX PR 02-SEP-1993; 93US-0116539.

XX PA (SLOA/) SLOANE N H.

XX PI Sloane NH;

XX DR WPI; 1994-100399/12.

XX PT Partial free N-terminal sequence of antineoplastic urinary protein -
useful for cancer therapy

XX PS Claim 2; Column 6; 4pp; English.

XX CC The invention relates to the elucidation of the partial N-terminal
XX CC amino acid sequence of antineoplastic urinary protein (ANUP). This
XX CC antitumour cytokine is present in human granulocytes and is excreted
XX CC from the serum into the urine. The protein contains a blocked N-terminal
XX CC amino acid, the blocking group of which has been identified as a
XX CC pyroglutamyl residue. The electrophoretically homogeneous ANUP (monomer
XX CC 16 kD) is treated with pyroglutamyl aminopeptidase to liberate the free
XX CC N-terminal amino group. The deblocked protein is transblotted and the
XX CC amino acid sequence of the electrophoretically homogeneous deblocked
XX CC protein is determined. It is found to be Leu-Lys-Cys-Tyr-Thr-Cys-Lys-
XX CC Glu-Pro-Met-Thr-(Thr or Ser)-Ala-Ala. ANUP may be utilised as a potential
XX CC antitumour chemotherapeutic agent to treat human neoplastic disease, as
XX CC it is non-toxic to human cells, specifically inhibits only human cancer
XX CC cell lines and causes regression of human tumour cell lines implanted in
XX CC nude mice.

XX CC The present sequence represents one of the two possibilities of the
XX CC deblocked N-terminal sequence as given above.

XX SQ Sequence 14 AA;

Query Match 84.8%; Score 78; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAA 15
|||||

Db 1 LKCYTCKEPMTXAA 15
|||||

RESULT 8
ABB37697

Db 1 LKCYTCKEPMTSAA 14

RESULT 7

AAW03298

ID AAW03298 standard; peptide; 14 AA.

XX AC AAW03298;

XX DT 22-DEC-1997 (first entry)

XX DE Antineoplastic urinary protein deblocked N-terminal sequence.

XX KW ANUP; antineoplastic urinary protein; cytokine; anticancer.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 12

XX FT /note= "it is unsure whether this residue is Thr or
Ser (see also AAW03299 and AAW03300)"

XX PN US5298604-A.

XX PD 29-MAR-1994.

XX PF 02-SEP-1993; 93US-0116539.

XX PR 27-JUL-1992; 92US-0919885.

XX PR 02-SEP-1993; 93US-0116539.

XX PA (SLOA/) SLOANE N H.

XX PI Sloane NH;

XX DR WPI; 1994-100399/12.

XX PT Partial free N-terminal sequence of antineoplastic urinary protein -
useful for cancer therapy

XX PS Claim 1; Column 6; 4pp; English.

XX CC The invention relates to the elucidation of the partial N-terminal
XX CC amino acid sequence of antineoplastic urinary protein (ANUP). This
XX CC antitumour cytokine is present in human granulocytes and is excreted
XX CC from the serum into the urine. The protein contains a blocked N-terminal
XX CC amino acid, the blocking group of which has been identified as a
XX CC pyroglutamyl residue. The electrophoretically homogeneous ANUP (monomer
XX CC 16 kD) is treated with pyroglutamyl aminopeptidase to liberate the free
XX CC N-terminal amino group. The deblocked protein is transblotted and the
XX CC amino acid sequence of the electrophoretically homogeneous deblocked
XX CC protein is determined. It is found to be Leu-Lys-Cys-Tyr-Thr-Cys-Lys-
XX CC Glu-Pro-Met-Thr-(Thr or Ser)-Ala-Ala. ANUP may be utilised as a potential
XX CC antitumour chemotherapeutic agent to treat human neoplastic disease, as
XX CC it is non-toxic to human cells, specifically inhibits only human cancer
XX CC cell lines and causes regression of human tumour cell lines implanted in
XX CC nude mice.

XX CC The present sequence represents one of the two possibilities of the
XX CC deblocked N-terminal sequence as given above.

XX SQ Sequence 14 AA;

Query Match 81.5%; Score 75; DB 15; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.7e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAA 15
|||||

Db 1 LKCYTCKEPMTXAA 14
|||||

ID	ABB37697 standard; Peptide; 558 AA.
XX	
AC	ABB37697;
XX	
DT	04-FEB-2002 (first entry)
XX	
DE	Peptide #5203 encoded by human foetal liver single exon probe.
XX	
KW	Human; foetal liver; gene expression; single exon nucleic acid probe.
XX	
OS	Homo sapiens.
XX	
PN	WO200157277-A2.
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US00669.
XX	
PR	04-FEB-2000; 2000US-0180312.
XX	
PR	26-MAY-2000; 2000US-0207456.
XX	
PR	30-JUN-2000; 2000US-0608408.
XX	
PR	03-AUG-2000; 2000US-0632366.
XX	
PR	21-SEP-2000; 2000US-0234687.
XX	
PR	27-SEP-2000; 2000US-0236359.
XX	
PR	04-OCT-2000; 2000GB-0024263.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-483447/52.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
XX	
PS	Claim 27; SEQ ID NO 30332; 639pp + sequence listing; English.
CC	The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 558 AA;
	Query Match 63.0%; Score 58; DB 22; Length 558; Best Local Similarity 64.3%; Pred. No. 1.4; Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps
QY	3 KCYTCKEPMTSNAC 16 : :
DB	285 KYKCGKPFSSAC 298
RESULT 9	
ABG03917	
ID	ABG03917 standard; Protein; 739 AA.
XX	
AC	ABG03917;
XX	
DT	13-FEB-2002 (first entry)
XX	
DE	Novel human diagnostic protein #3908.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
XX	
OS	Homo sapiens.
XX	

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PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX N-PSDB; ABL12332.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Disclosure; SEQ ID NO 31479; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB116176-AB116175), expressed DNA
XX sequences (AB116176-AB116175) and the encoded proteins
XX (AB116176-AB116175).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 2931 AA;
XX
XX Query Match 56.5%; Score 52; DB 22; Length 2931;
XX Best Local Similarity 47.4%; Pred. No. 61;
XX Matches 9; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
XX
XX Qy 2 LKCYTCKEPM---TSAAC 16
XX :|||||:|:|:|
XX 1411 LECYTCXDPFCEDPTTSKC 1429
XX
XX
XX RESULT 11
XX AAM99933
XX ID AAM99933 standard; Protein; 212 AA.
XX
XX AC AAM99933;
XX
XX DT 07-JAN-2002 (first entry)
XX
XX DE Human polypeptide SEQ ID NO 49.
XX
XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX KW vulnarly; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; human; secreted protein.
XX
XX OS Homo sapiens.
XX
XX PN W0200155173-A2.
XX
XX PD 02-AUG-2001.
XX
XX PF 17-JAN-2001; 2001WO-US01356.
XX
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX

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PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 22-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0234998.
PR 27-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.

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PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-451924/48.
XX N-PSDB; AA199531.
XX
XX New nucleic acids and polypeptides, useful for treating, preventing or
XX ameliorating human disorders and diseases -
XX
XX Claim 11; SEQ ID NO 49; 465pp + Sequence Listing; English.
XX
XX The invention relates to novel human polynucleotides (AA199513-AA199538)
XX and the encoded proteins (AAM99915-AAM99934) which are useful for
XX preventing, treating or ameliorating medical conditions e.g. by protein

CC or gene therapy. The genes are isolated from a range of human tissues
CC disclosed in the specification. The nucleic acids, proteins, antibodies
CC and (ant)agonists are useful in the diagnosis, treatment and prevention
CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC myocardial ischaemias; (d) wound healing; (e) neurological diseases
CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as
CC viral, bacterial, fungal and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX

XX Sequence 212 AA;

Query Match 54.3%; Score 50; DB 22; Length 212;
Best Local Similarity 53.8%; Pred. No. 8.6;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPTMTSAAC 16
|:|:|:|:|:
Db 172 CFTCQEPPTSTGC 184

RESULT 12

AAM99920

ID AAM999920 standard; Protein; 272 AA.

XX
AC AAM999920;

XX
DT 07-JAN-2002 (first entry)

XX
DE Human polypeptide SEQ ID NO 36.

XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antifungal; antitumor;
KW vulvar; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.

OS Homo sapiens.

XX
XX WO200155173-A2.

XX
PD 02-AUG-2001.

XX
PF 17-JAN-2001; 2001WO-US01356.

XX
PR 31-JAN-2000; 2000US-0179065.

PR
PR 04-FEB-2000; 2000US-0180628.

PR
PR 24-FEB-2000; 2000US-0184664.

PR
PR 02-MAR-2000; 2000US-0186350.

PR
PR 16-MAR-2000; 2000US-0189874.

PR
PR 17-MAR-2000; 2000US-0190076.

PR
PR 18-APR-2000; 2000US-0198123.

PR
PR 19-MAY-2000; 2000US-0205515.

PR
PR 07-JUN-2000; 2000US-0209467.

PR
PR 28-JUN-2000; 2000US-0214886.

PR
PR 30-JUN-2000; 2000US-0215135.

PR
PR 07-JUL-2000; 2000US-0216647.

PR
PR 07-JUL-2000; 2000US-0216880.

PR
PR 11-JUL-2000; 2000US-0217487.

PR
PR 14-JUL-2000; 2000US-0217496.

PR
PR 26-JUL-2000; 2000US-0218290.

PR
PR 26-JUL-2000; 2000US-0220963.

PR
PR 14-AUG-2000; 2000US-0224518.

PR
PR 14-AUG-2000; 2000US-0224519.

PR
PR 14-AUG-2000; 2000US-0225213.

PR
PR 14-AUG-2000; 2000US-0225214.

PR	14-AUG-2000;	2000US-0225266.
PR	14-AUG-2000;	2000US-0225267.
PR	14-AUG-2000;	2000US-0225268.
PR	14-AUG-2000;	2000US-0225270.
PR	14-AUG-2000;	2000US-0225447.
PR	14-AUG-2000;	2000US-0225757.
PR	14-AUG-2000;	2000US-0225758.
PR	14-AUG-2000;	2000US-0225759.
PR	18-AUG-2000;	2000US-0226279.
PR	22-AUG-2000;	2000US-0226681.
PR	22-AUG-2000;	2000US-0226686.
PR	22-AUG-2000;	2000US-0227182.
PR	23-AUG-2000;	2000US-0227009.
PR	30-AUG-2000;	2000US-0228924.
PR	01-SEP-2000;	2000US-0229287.
PR	01-SEP-2000;	2000US-0229343.
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PR	05-SEP-2000;	2000US-0229509.
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PR	06-SEP-2000;	2000US-0230437.
PR	06-SEP-2000;	2000US-0230438.
PR	08-SEP-2000;	2000US-0231242.
PR	08-SEP-2000;	2000US-0231243.
PR	08-SEP-2000;	2000US-0231244.
PR	08-SEP-2000;	2000US-0231413.
PR	08-SEP-2000;	2000US-0231414.
PR	08-SEP-2000;	2000US-0232080.
PR	08-SEP-2000;	2000US-0232081.
PR	12-SEP-2000;	2000US-0231968.
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PR	14-SEP-2000;	2000US-0232400.
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PR	14-SEP-2000;	2000US-0233064.
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PR	21-SEP-2000;	2000US-0234223.
PR	21-SEP-2000;	2000US-0234274.
PR	25-SEP-2000;	2000US-0234997.
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PR	27-SEP-2000;	2000US-0235834.
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PR	29-SEP-2000;	2000US-0236327.
PR	29-SEP-2000;	2000US-0236367.
PR	29-SEP-2000;	2000US-0236368.
PR	29-SEP-2000;	2000US-0236369.
PR	29-SEP-2000;	2000US-0236370.
PR	02-OCT-2000;	2000US-0236802.
PR	02-OCT-2000;	2000US-0237037.
PR	02-OCT-2000;	2000US-0237038.
PR	02-OCT-2000;	2000US-0237039.
PR	13-OCT-2000;	2000US-0237040.
PR	13-OCT-2000;	2000US-0239935.
PR	13-OCT-2000;	2000US-0239937.
PR	20-OCT-2000;	2000US-0240960.
PR	20-OCT-2000;	2000US-0241221.
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PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
PR	20-OCT-2000;	2000US-0241808.
PR	20-OCT-2000;	2000US-0241809.
PR	20-OCT-2000;	2000US-0241826.
PR	08-NOV-2000;	2000US-0244617.
PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	08-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
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PR	17-NOV-2000;	2000US-0249215.
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PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	200

SQ Sequence 272 AA;
 Query Match 54.3%; Score 50; DB 22; Length 272;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPTSAAC 16
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 Db 172 CFTCQEPSTGTC 184

RESULT 13
 ABU11798
 ID ABU11798 standard; Protein; 514 AA.
 AC ABU11798;
 XX
 XX 13-FEB-2003 (first entry)
 DT
 DE Human MDDT polypeptide SEQ ID 745.
 XX
 KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianemic; antipsoriatic; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200279449-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US09944.
 XX
 XX 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299776P.
 PR 20-JUN-2001; 2001US-300001P.
 XX
 (INCY-) INCYTE GENOMICS INC.
 XX
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Anshey SR;
 PI Daugherty SC, Dam TC, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 DR WPI; 2003-058431/05.
 DR N-PSDS; ABX34788.
 XX
 XX New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis -
 XX
 XX Claim 27; SEQ ID NO 745; 339pp + Sequence Listing; English.
 XX
 XX This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianemic, antipsoriatic and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are

CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
 CC by ABU11450-ABU11845, described in the disclosure of the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 514 AA;
 Query Match 54.3%; Score 50; DB 24; Length 514;
 Best Local Similarity 53.8%; Pred. No. 21;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPTSAAC 16
 :||:|
 Db 175 CFTCQEPSTGTC 187

RESULT 14
 ABU12085
 ID ABU12085 standard; Protein; 612 AA.
 XX
 AC ABU12085;
 XX
 XX 19-FEB-2003 (first entry)
 DT
 DE Human NOV26a CG93871-01 protein SEQ ID 90.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiac;
 KW antilipaeamic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200281625-A2.
 PN
 XX
 PD 17-OCT-2002.
 XX
 XX 03-APR-2002; 2002WO-US10366.
 PF
 XX 03-APR-2001; 2001US-281086P.
 PR 05-APR-2001; 2001US-281906P.
 PR 06-APR-2001; 2001US-282020P.
 PR 10-APR-2001; 2001US-282930P.
 PR 12-APR-2001; 2001US-283444P.
 PR 12-APR-2001; 2001US-283512P.
 PR 13-APR-2001; 2001US-283657P.
 PR 13-APR-2001; 2001US-283678P.
 PR 13-APR-2001; 2001US-283710P.
 PR 17-APR-2001; 2001US-284234P.
 PR 19-APR-2001; 2001US-285325P.
 PR 20-APR-2001; 2001US-285381P.
 PR 24-APR-2001; 2001US-286068P.
 PR 25-APR-2001; 2001US-286292P.
 PR 07-JUN-2001; 2001US-296692P.
 PR 26-JUN-2001; 2001US-300883P.
 PR 08-AUG-2001; 2001US-311003P.
 PR 13-AUG-2001; 2001US-311973P.
 PR 16-AUG-2001; 2001US-312901P.
 PR 14-SEP-2001; 2001US-322283P.
 PR 05-OCT-2001; 2001US-327448P.
 PR 31-DEC-2001; 2001US-345734P.
 PR 03-JAN-2002; 2002US-345755P.
 PR 04-FEB-2002; 2002US-354391P.
 PR 02-APR-2002; 2002US-0114153.

XX PA (CURA-) CURAGEN CORP.
 XX PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G;
 PI Guo X, Gerlach V, Caaman SJ, Boldog FL, Li L, Zerhusen BD;
 PI Thernevi VI, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM;
 PI Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA;
 PI Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A;
 XX WPI: 2003-046862/04.
 DR N-PSDB: ABX56305.
 XX
 XX New isolated NOVX polypeptide useful for treating cardiomyopathy,
 PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
 PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
 PT cancer -
 XX Claim 1; Page 188; 425pp; English.
 XX
 XX This invention describes novel polypeptides, termed NOVX which have
 CC anti-diabetic, anti-arteriosclerotic, anorectic, metabolic, antimicrobial,
 CC neuroprotective, anti-parkinsonian, antilipemic, cyostatic, nootropic,
 CC cardiant and immunomodulatory activity. The polypeptide and any
 CC antibodies generated from it are useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease
 CC selected from a pathology associated with the NOVX polypeptide. Fragments
 CC and portions of the polynucleotides encoding NOVX polypeptides are useful
 CC to map the location of NOVX genes on a chromosome, to identify
 CC individuals from minute biological samples, as DNA markers for
 CC restriction fragment length polymorphism (RFLP), and are useful to
 CC prepare polymerase chain reaction primers. The products of the invention
 CC can be used in gene therapy and for treating cardiomyopathy, metabolic
 CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
 CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
 CC disease, immune disorders, haematopoietic disorders, and various
 CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
 CC syndrome X and wasting disorders associated with chronic diseases and
 CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
 CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306.
 XX
 XX Sequence 612 AA;
 SQ
 Query Match 54.3%; Score 50; DB 24; Length 612;
 Best Local Similarity 53.8%; Pred. No. 25;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 4 CYTCKEPTMTSAAC 16
 Db 547 CFTCQEPPTSGC 559
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 |||||
 RESULT 15
 AAG66137
 ID AAG66137 standard; Protein; 240 AA.
 XX AA:66137;
 AC
 XX 13-MAR-2002 (first entry)
 DT Human MFQ-110 polypeptide.
 DE
 XX Zinc finger protein; MFQ-110; developmental disorder; neurodegenerative;
 KW psychiatric; vascular disease; angiogenesis; cancer; human.
 XX Homo sapiens.
 OS
 XX WO200185765-A2.
 PN
 XX 15-NOV-2001.
 PD
 XX 11-MAY-2001; 2001WO-EP05372.
 PF
 XX 12-MAY-2000; 2000EP-0110089.
 PR

XX PA (MERE) MERCK PATENT GMBH.
 XX PI Rodas Gubern B, Messeguer Peypoch R, Masa Alvarez M, Rosell Vives E;
 XX WPI: 2002-055583/07.
 DR N-PSDB; AAI67913.
 XX
 XX Identification of a new human C2H2-type finger protein, MFQ-110, which
 PT may be useful in the treatment and diagnosis of disease such as
 PT developmental disorders, neurodegenerative disease, vascular disease
 PT and cancer -
 XX Claim 1; Page 60-61; 63pp; English.
 XX
 XX The invention provides new human C2H2-type zinc finger proteins, MFQ-110.
 CC The MFQ-110 polypeptides can be expressed by standard recombinant
 CC methodology. The MFQ-110 polypeptides and polynucleotides can be used in
 CC diagnostic assays for detection of abnormally decreased or increased
 CC levels of polypeptide or mRNA expression. This may be used for diagnosing
 CC or determining susceptibility of a subject to diseases that include
 CC developmental disorders, neurodegenerative disease, brain stroke,
 CC psychiatric disorders such as schizophrenia, cardiac and vascular
 CC disease, angiogenesis and cancer especially lymphomas. The polypeptides
 CC may be used to identify membrane bound or soluble receptors and may be
 CC used to identify agonists and antagonists which compete with receptor
 CC binding. The polynucleotides may be used as diagnostic reagents through
 CC detecting mutations in the associated gene, for chromosome localization
 CC studies and tissue expression studies. The present sequence represents a
 CC human MFQ-110 polypeptide.
 XX
 XX Sequence 240 AA;
 SQ
 Query Match 52.2%; Score 48; DB 23; Length 240;
 Best Local Similarity 72.7%; Pred. No. 20;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CYTCKEPTMTSA 14
 Db 172 CTTCCKQPTTSA 182
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